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OM nucleic - nucleic search, using bw model

Run on: January 15, 2004, 06:08:59 ; Search time 2613 Seconds
(without alignments)
1807.571 Million cell updates/sec

Title: US-09-809-545A-1

Perfect score: 1340
Sequence: 1 ggcggccggccggccgacacacat.....ggcgaagggttcgctaga 1340

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1340	100.0	1340	10	US-09-809-545A-1	Sequence 1, Appli
2	857.2	64.0	2372	9	US-09-794-591-1	Sequence 1, Appli
3	275.6	20.6	1506	13	US-10-359-385-5	Sequence 5, Appli
4	274	20.4	1558	13	US-10-094-749-287	Sequence 287, App
5	261	19.5	1843	11	US-09-919-039-266	Sequence 266, App
6	123.8	9.2	473	9	US-09-864-761-11804	Sequence 11804, A
7	109.6	8.2	125	9	US-09-864-761-28375	Sequence 28375, A
8	90.4	6.7	255	13	US-10-029-386-26399	Sequence 26399, A
9	90.4	6.7	502	13	US-10-029-386-12653	Sequence 12659, A
10	88	6.6	224	9	US-09-864-761-22653	Sequence 22653, A
11	86.4	6.4	454	9	US-09-864-761-5893	Sequence 5893, Ap
12	58	4.3	2350	12	US-10-292-798-1837	Sequence 1837, Ap
13	58	4.3	2350	13	US-10-017-161-2191	Sequence 2191, Ap
14	57	4.3	65	13	US-09-908-975-27923	Sequence 27923, A
15	55.8	4.2	6668	13	US-10-311-455-1669	Sequence 1669, Ap

16	55.2	4.1	60	13	US-09-908-975-7420	Sequence 7420, Ap
17	55.2	4.1	3001	15	US-10-172-086-57	Sequence 57, Appl
18	55.2	4.1	4722	13	US-10-311-455-2037	Sequence 2037, Ap
19	53.6	4.0	9539	13	US-10-240-453-54	Sequence 54, Appl
20	53.6	4.0	9539	13	US-10-239-676-52	Sequence 52, Appl
21	53.4	4.0	5464	13	US-10-311-455-1889	Sequence 1889, Ap
22	53	4.0	1223197	13	US-10-027-632-179264	Sequence 179264, A
23	53	4.0	1223197	14	US-10-027-632-179264	Sequence 53, Appl
24	52.8	3.9	396	9	US-09-825-294-53	Sequence 53, Appl
25	52.8	3.9	396	12	US-10-369-186-53	Sequence 53, Appl
26	52.8	3.9	396	12	US-10-361-811-53	Sequence 53, Appl
27	52.8	3.9	396	16	US-10-212-677-53	Sequence 2148, Ap
28	52.8	3.9	113515	13	US-10-311-455-2148	Sequence 4582, Ap
29	52.6	3.9	113515	13	US-09-960-352-4582	Sequence 20, Appl
30	52	3.9	393	10	US-10-312-841-20	Sequence 2, Appli
31	52	3.9	3673778	13	US-09-918-995-16144	Sequence 16144, A
32	51.6	3.9	461	11	US-09-918-995-16144	Sequence 32216, A
33	51.6	3.9	495	11	US-10-128-714-7140	Sequence 7140, Ap
34	51.6	3.8	1347	15	US-10-311-455-474	Sequence 1541, Ap
35	51.2	3.8	5314	13	US-10-240-452-10	Sequence 10, Appl
36	51	3.8	5314	13	US-10-311-455-1541	Sequence 474, App
37	51	3.8	8305	13	US-10-311-455-1541	Sequence 2147, Ap
38	51	3.8	8342	13	US-10-311-455-2147	Sequence 144, App
39	51	3.8	113515	12	US-10-085-117-241	Sequence 1377, Ap
40	51	3.8	165961	12	US-10-311-455-144	Sequence 1692, Ap
41	51	3.8	3973	13	US-10-311-455-1377	Sequence 1056, Ap
42	50.4	3.8	16033	13	US-10-311-455-1692	
43	50.4	3.8	17934	13	US-10-311-455-1056	
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ALIGNMENTS

RESULT 1
US-09-809-545A-1
; Sequence 1, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS.017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-809-545A-1

QY	1	GGGCGCGCCCTGACACATAGCTTATGCTTCAGCGGAGTTCCTCCACCCAG	60
DB	1	GGGCGCGCCCTGACACATAGCTTATGCTTCAGCGGAGTTCCTCCACCCAG	60
QY	61	ATGGGATCTGAGATACAGGCGCCCTCATCCCATCCCGGCGAGAGACACCGGCGAG	120
DB	61	ATGGGATCTGAGATACAGGCGCCCTCATCCCATCCCGGCGAGAGACACCGGCGAG	120
QY	121	CCCACTGTCCTCCGACACATTAATGATCTCTTACACAGACGACTCGAGACAG	180
DB	121	CCCACTGTCCTCCGACACATTAATGATCTCTTACACAGACGACTCGAGACAG	180
QY	181	CGCTTATACAGCGACGCGCTTTCGCGACCGACACAGACGATGATCCGCGCG	240
DB	181	CGCTTATACAGCGACGCGCTTTCGCGACCGACACAGACGATGATGCGCGCG	240


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QY 592 GTGGGCGCGCTACAGCCCGGACCTTCTATGACAGGACGGTGTGTGTGTCAGGCCAAC 651
DB 1629 GTGGGTGCACTACAGTCCCGAATTTCTATGACAGGACGGTGTGTGTGTCAGGCCAAC 1688
QY 652 CAGGAGGATCTTCCATGTAAGTGGCCCACTTCTATGTAATCTTGTGCAATGCTT 711
DB 1689 CAGGAGGATCTTCCATGTAAGTGGCCCACTTCTATGTAATCTTGTGCAATGCTT 1748
QY 712 GGGCTTCATATCGGCGCGCACTGTGCAAGTGTGCAATGCGAGGGGTGCACTTGTGAGGC 771
DB 1749 GGGCTTCATATCGGCGCGCACTGTGCAAGTGTGCAATGCGAGGGGTGCACTTGTGAGGC 1808
QY 772 CGTGTGCGACCGGTGTAACAACCTTGTGAGTGTGCGCGCCCGCCCAATCCGCGCC 831
DB 1809 CGGAGTGCACCGGTGTAACAACCTTGTGAGTGTGCGCGCCCGCCCGCCCGATCCGCGCC 1868
QY 832 TATGCGCGAGTGTATGTAAGAGCCAGTGTATGCAATTAATGCTTACAGGGTGTAT 891
DB 1869 TACGGCGGTGTGTATAC--CAGGATGATTTATGATGTCAGACATTTATGATGTTAT 1926
QY 892 GGTGCAATACCGGTACCGCGCGCAACCCCTGTGCACTGTGCTGCTTACAGTGA----- 944
DB 1927 GGTGCAATACCGGTACCGCGCGCAACCCCTGTGCACTGTGCTGCTTACAGTGA----- 944
QY 945 -----CAGTTACGAGCAG 958
DB 1987 CAGTTGCTTCTGTGAGAGAGATGAATTTCTTGTAAACCTGTGAGTTAGAGAGAG 2046
QY 959 TTTATGCTGCGACCCCTTACACCAACACTTGTCTTCCAGCCCGCCCTTACAGGGTGTG 1018
DB 2047 TTTATGCTGCGACCCCTTACACCAACACTTGTCTTCCAGCCCGCCCTTACAGGGTGTG 2106
QY 1019 CAGTGAATGTTTGTGCGCCCTTACAGGATGCGCAAGTGTGAGGACCAATGCTGATGATG 1078
DB 2107 CAGTGAATGTTTGTGCGCCCTTACAGGATGCGCAAGTGTGAGGACCAATGCTGATGATG 2166
QY 1079 GTCCTGTTCTTCTATGCACTGAGGCTATATACCAAGGGGATCAACCGTTGTCTC 1138
DB 2167 GTCCTGTTCTTCTATGCACTGAGGCTATATACCAAGGGGATCAACCGTTGTCTC 2226
QY 1139 CATATTAATGATTAACCATTAACCAACCAACCAACCAACCAACCAACCAACCAAC 1198
DB 2227 CATATTAATGATTAACCATTAACCAACCAACCAACCAACCAACCAACCAACCAAC 2250
QY 1199 CAACCTTCCATGTGGGAGAGAGAAAGCTTTCGAGGCCCGGAGTGTGCAACATGCA 1258
DB 2251 -AACCTTCCATGTGGGAGAGAGAAAGCTTTCGAGGCCCGGAGTGTGCAACATGCA 2309
QY 1259 GTAGGACATCACTTTAGCACTCAAGAAACAAAGAAAAAATTA 1318
DB 2310 GTAGGACATCACTTTAGCACTTTTAAAAAATTA 2369

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RESULT 3
US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication NO. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program

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; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-10-359-385-5

Query Match      20.6%; Score 275.6; DB 13; Length 1506;
Best Local Similarity 60.2%; Pred. No. 2,3e-67;
Matches 601; Conservative 0; Mismatches 354; Indels 43; Gaps 7;

QY 222 GACAGATGATGCGCGCCCGACCGACCGCCAGC---CCAGACACAACCTTGTGAAACAC 278
DB 452 GACAGAGGTGAGGACACAGACAGACCGCCAGCAGTGCAGACACAAAGTATGAAATTC 511
QY 279 AGAAAACAAGTCCAGCCCAAGCGGTGATGTGTCAATCCCTTCCGTTCCGGGA 338
DB 512 AGAGATTAATCTACCCCGAAACGGCTGATGTCTTAATATCTTCCGCTCCGGGA 571
QY 339 TCCAGACCTCCGACAAATGTTGGCCAAATTTGTAATAATTAATTAATTT 398
DB 572 CCTGACCTCCGACAGATGTTGGCAGTTTGCAAAATCTTATGATGTAATTAATTT 631
QY 399 TATGACCGGGCTCGAAGGATTTGTTCTGTAATCTTGAATAATGTCGAGATGCGGA 458
DB 632 TATGACCGGTGCTTAAGGATTTGGGTTCTGTAATCTTGAATAATGTCGAGATGCGGA 691
QY 459 CAGGGGAGGAGAAATTCACGATCCGTGTAGAGGGCCGTAATATGAGGTTAATA 518
DB 692 CAGGGGAGGAGAAATTCACGATCCGTGTAGAGGGCCGTAATATGAGGTTAATA 751
QY 519 TCGCAGACGCGGTGATGATTAATAAAGGCGGTGAACCCCTCACCAATGGCTGGA 578
DB 752 TGTACAGCAGTGTATATACCAATAGAAAGTGTCAACATATGCAATATGTTGGA 811
QY 579 ATTAAATCCAGTGTGTGGCGCGCTACAGCCCGCACTTCTATGAG-----GCA 628
DB 812 ATTAAATCCAGTGTGTGGCGCGCTACAGCCCGCACTTCTATGAG-----GCA 871
QY 629 CGGTGCTGTGTGCGAGGCAACAGAGGAGTCTTCCATGTA--CAGTGGCCCAATTC 686
DB 872 AGCAGATGTGCTTACAGGCAATGATGACAGTGGCCCTATCAGGAAGAGGGGATCA 931
QY 687 ACTTGATATATCTTGTGCAATGCTGCTTTCATA---TCCGCGCCCACTGCGAGC 743
DB 932 CACTTACATTTCTTAAATCATTTCTGCTTCCCTTACCTTACAGCCACAGCGAGC 991
QY 744 TGCATACCGAGGGGCTCACTTTCAGAGCCGTGTGCAACCTGTACCAACCTTCAAGAGC 803
DB 992 CGCTTTCAGAGGAGCCCATTTTACAGGGGAGAGGGGCGGACAGTATATGTGCACTCGA-- 1049
QY 804 TCGGCGCGCCCAACCCCAATCCGCGCTTATGCGGAGTGTATCAAGACCAAGTGA 863
DB 1050 -CGGTACCTCCAAAGCCATCCCGCTATCAGGGGAGATATGACGCTTACAG----- 1104
QY 864 TGGCAATTAATGTCTACAGGGGTGTACGCTGTACATCCGCTACGCCCAACCCCTGCG 923
DB 1105 -----ATATGACAGCCTGTCTATCTCAACCGAGCCACCGCTGTGCGAGC 1149
QY 924 CACTGCTGTGCTACAGTACAGTACGAGTGAAGATTTATGTGCGCACCCCTTACACCA 983
DB 1150 CGCTGACAGCGCTTACAGTACAGTGTATGAGGGGTGTATCAAGCGACCCCTTACATGCG 1209
QY 984 CACTTGTCTCAGCCCGCACTTACAGCGGTGTGTGCTTATGCTTTTGGCGCCCTTAC 1043
DB 1210 C---CTTGCCTTGCCTGCTAGCTATGAGTGTGCGCTGTGCGAGTATATACCGAGTGG 1266
QY 1044 CGATGCCAAGACTAGAGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 1103
DB 1267 CTACAGCGATTTGCCCTTACTGATGATGATGATGATGATGATGATGATGATGATGATG 1326
QY 1104 TAGTATATACCAAGGGGATACCAACCGTTTGTGCTCATATTAATTAATTAATTAATTA 1163

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Db 1327 CAGTTTCATGAGGCGCTATTGCAATTTTACTTGTAGAGAACTTATTCGAAAGATGA 1386
 QY 1164 CAAACAGCAAAAAACAAACAAAAACAAAAACCAA 1201
 Db 1387 AGAGAAAAACAAACAAACAAACAAACAAACACAAA 1424

RESULT 4

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US-10-094-749-287
: Sequence 287, Application US/10094749
: Publication No. US20030219741A1
: GENERAL INFORMATION:
: APPLICANT: ISOGAI, TAKAO
: APPLICANT: SUGIYAMA, TOMOYASU
: APPLICANT: OTSUKI, TETSUJI
: APPLICANT: MAKAMATSU, AI
: APPLICANT: SATO, HIROYUKI
: APPLICANT: ISHII, SHIZUKO
: APPLICANT: YAMAMOTO, JUN-ICHI
: APPLICANT: ISONO, YUUKO
: APPLICANT: HIO, YURI
: APPLICANT: OTSUKA, KAORU
: APPLICANT: NAGAI, KEIICHI
: APPLICANT: IRIE, RYOTARO
: APPLICANT: TAMECHIKA, ICHIRO
: APPLICANT: SEKI, NAOHICO
: APPLICANT: YOSHIKAWA, TSUTOMU
: APPLICANT: OTSUKA, MOTOTYUKI
: APPLICANT: NAGAHARI, KENJI
: APPLICANT: MASUHO, YASUHIKO
: TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
: FILE REFERENCE: 084335/0160
: CURRENT APPLICATION NUMBER: US/10/094, 749
: CURRENT FILING DATE: 2002-03-12
: PRIOR APPLICATION NUMBER: 60/350, 435
: PRIOR FILING DATE: 2002-01-24
: PRIOR APPLICATION NUMBER: JP 2001-328381
: PRIOR FILING DATE: 2001-09-14
: NUMBER OF SEQ ID NOS: 3361
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 287
: LENGTH: 1558
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-094-749-287

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Query Match	20.4%	Score 274;	DB 13;	Length 1558;
Best Local Similarity	65.2%;	Pred. No. 6.6e-67;		
Matches 558; Conservative	0;	Mismatches 235;	Indels 63;	Gaps 8

Oy	222	GACAGATGATCGCGCCCGACCGACGGCGAGCAGC	278
Db	538	GACGGAAGGTGGAGCAGACAGACGGCGAGTCA	597
Oy	279	AGAAAACAAGTCCACGCGCGCTGATGTGCCA	338
Db	598	AGAGGTAAATCTACCCGAAACGGCTCAATCT	657
Oy	339	TCCAGCCTCGACAAATGTTGGCAAATTTGTA	398
Db	658	CCCTGACCTCGCGCAGATGTTGGCAATTTG	717
Oy	399	TAAATGAGCGGGCTCGAAGGGATTTGGTTG	458
Db	718	TAAATGAAGTGGCTCTTAAGGATTCGGGTC	777
Oy	459	CAGGCGCAGGGAGAAATTCACGCTACCGTGA	518
Db	778	CAGGGCCAGGGAGAAATTCACGCGACCGTGT	837
Oy	519	TGCGACAGCAGCGCTGATGACTTAATPAAA	578

Db	838	TGCTACAGCAGCGTGATATGACCAATAGAAGATGCTCACACATATCAATGATTGAA	897
Qy	579	ATTAAATCCAGTGTGTGGCGCGGTCTACACCCCGACTTCTATGCA-----GCA	628
Db	898	ATTAAAGCCAGTAGTGGAGCTGATATATGATTCGGAGATTATATGACAACTTCAGCTTTCA	957
Qy	629	CGGTGCTGTGTGTCAGAGCCAAACAGAGAGGATCTTCATGTA-----CAG	674
Db	958	AGCAGATGTGTCTTAAAGCAATGATGACAGCTGCCCTTATCAGAAAGAGGGGTATCA	1017
Qy	675	TGGCCCAAGTTCACCTTGATATATCTTTCGCAATGCTCGCTTTCATA---TCCGAGCG	731
Db	1018	CACCTAATATTCCTTTATCAGTCTCCTTTTAGTTCCTGGCTCCCTTAACCTACTGAGC	1077
Qy	732	CACGTCTGCACTGTCATACCGAGGGGCTCACCTTCAGGCCGTGTGTGCACCGTGTACAA	791
Db	1078	CACCAACGAGCGCGCTTTCAGAGAGCCCATTTGAGGGGAGAGGGCGGACAGATATATGG	1137
Qy	792	CACCTTACAGCTGCGCGCGCCCAACCCCAATCCCGGCTTATGAGGAGATAGTATCA	851
Db	1138	TGCAGTCCGA---GCGGTACCTCCAAAGCCATCCCGCTATCCAGGTGTGTTACCA	1194
Qy	852	AGAGCCAGTGATATGACATAAATTGTACAGGGGTGTTCAGCTGATACCGCTACGCCCA	911
Db	1195	GGAGCGATTTTACGCTGCTGA---CCTCTATGTGTGATATGCACTTACAGATATGACA	1251
Qy	912	GCCCAACCCCT-----GCCACTGTCTGCTGCTTACAGTGAAG	947
Db	1252	GCCTGTACACTGCAACGCGACGACCGGTGTGACGCGGTGACGCGCTTACGGTGAAG	1311
Qy	948	TTTACGACGAGTTTATGTCTGCCGACCCCTTACACACACACACTTGTCTCAGGCCCACTTA	1007
Db	1312	TTTATGGCAGGGTGTACACAGCCGACCCCT---ACATGACCTTTCCTCCTGCGCTAGCTA	1368
Qy	1008	CGCGCTGTGTGCATG	1023
Db	1369	TGAGATTGGCGCTGTG	1384

RESULT 5

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US-09-919-039-266
; Sequence 266, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaest, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 266
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 253783.3
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1824
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-266

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Query Match	19.5%	Score 261;	DB 11;	Length 1843;
Best Local Similarity	68.8%	Pred. No. 3.6e-63;		
Matches 433; Conservative	0;	Mismatches 185;	Indels 11;	Gaps 5;

Oy 34 CCTCAGGCGCAATTGCTCCACCCGAGATGGCAT-CCTGCAGATTACCGGCCCCCTCATC 92
 Db 716 CCGCGCAGTACCCCCCTTCCGCCAAGAACGGATCCTGCGCGATTAGGCCCCGCGCCCAAC 775

QY	93	CCGATTCGGCGCCAGA -GACACCGGCCAGGCCCACTGTGCC-----GCCACACATTAAAC	146
Db	776	CGACCCCGACGAGAGTACTCTCGGCCAGACCCCGTCTCCACAGAGCATGGCATGACCC	835
QY	147	TTGATCTCTCTACACAGCGCACTCGAGCAG--AGCGTTTATCAAGCGACAG-CCG	202
Db	836	TGTACACACCGACGACGACCCACCCCGAGGACGAGCTCCGAGGCGACGACGACGCCA	895
QY	203	TCTTCGCGACCGCCACACAGACAGATGATCGCGCCCGACCGAGCGGCCACGCCGACAC	262
Db	896	TCGCGCGGAGCCCGACAGCATGTCCGACACACAGAGCGGCGACAGACGACGACGCCG	955
QY	263	AACCTTTGAAANACAGAAAACAAGTCCAGGCCCAAGCGGCTGCATGTGTCCACATCC	322
Db	956	TCACCCCTCCGACCTTACAGAGAGAGCAGCCCAAGCGGCTACACGCTCCACATCC	1015
QY	323	CCTTCGGGTTCCGGGATCCAGACCTCCGACAAATGTTGGCCATTTGGTAAATATTAG	382
Db	1016	CTTTCGGGTTCCAGGACCCCGACTGTGGGCAATTTTCGGGCAATTCGAAAAATTTTNG	1075
QY	383	ATGTTGAAATTAATTTTAAATGAGCGGGCTCGAAGGAGTTTGTTCGTACTTTGAAA	442
Db	1076	ACGTGAGATCATTTTAAAGAGGGGGCTCAAGGATTTTGGGTTTGTAACTTTGAAA	1135
QY	443	ATAGTGGGATTCGCGACAGGGCCGAGGAGAAATTGACAGTACCGTGTGTAGAGGCCGTA	502
Db	1136	CTAGCTAGATGCTGACCGAGCCCGGAGAAAGCTGATGTGGAGCATGCTGAGGGAGCGGA	1195
QY	503	AAATCGAGTTTAATTAATGACAGACAGCGGTGATGACTAATAAAAAAGCGTGAACCCCT	562
Db	1196	AAATTTGGTCAATTAATGACAGCGCCGAGTGTATGACACAGAGAGACGGGGAACCCCT	1255
QY	563	ACAACCAATGCGTGAATTAATTAATCCAGTTGTGGCGCGGTCTACAGACCCCGACTTATG	622
Db	1256	ACACCAACGGCTGGAACTTAATTCAGTGTGTGGCGCAGTCTACAGGCGCTGAATTTATG	1315
QY	623	CAGGACACGGTGTGTGTGTGTCAGGCCAC	651
Db	1316	CAGTGACGGGGTTCCTCCCTACCCACACACC	1344
RESULT 6			
US-09-864-761-11804			
Sequence 11804, Application US/09864761			
Patent No. US20020048763A1			
GENERAL INFORMATION:			
APPLICANT: Penn, Sharon G.			
APPLICANT: Rank, David R.			
APPLICANT: Hanzel, David K.			
APPLICANT: Chen, Wensheng			
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR			
FILE REFERENCE: Aeomica-X-1			
CURRENT APPLICATION NUMBER: US/09/864,761			
CURRENT FILING DATE: 2001-05-23			
PRIOR APPLICATION NUMBER: US 60/180,312			
PRIOR FILING DATE: 2000-02-04			
PRIOR APPLICATION NUMBER: US 60/207,456			
PRIOR FILING DATE: 2000-05-26			
PRIOR APPLICATION NUMBER: US 09/632,366			
PRIOR FILING DATE: 2000-08-03			
PRIOR APPLICATION NUMBER: GB 24263.6			
PRIOR FILING DATE: 2000-10-04			
PRIOR APPLICATION NUMBER: US 60/236,359			
PRIOR FILING DATE: 2000-09-27			
PRIOR APPLICATION NUMBER: PCT/US01/00666			
PRIOR FILING DATE: 2001-01-30			
PRIOR APPLICATION NUMBER: PCT/US01/00667			
PRIOR FILING DATE: 2001-01-30			
PRIOR APPLICATION NUMBER: PCT/US01/00664			
PRIOR FILING DATE: 2001-01-30			
PRIOR APPLICATION NUMBER: PCT/US01/00669			

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PRIORITY FILLING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILLING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILLING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILLING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILLING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILLING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILLING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILLING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/508,408
PRIORITY FILLING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11804
LENGTH: 473
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: MAP TO AC006075.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.57
US-09-864-761-11804

Query Match
Best Local Similarity 9.2%; Score 123.8; DB 9; Length 473;
Matches 131; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 220 CAGACGATGATGCCGCCGCCGACCGACGCGCCAGCCCAAGACACACCTTTGAAAAACA 279
DB 269 CAGACGATGACGCGACGACACCGACGATGCGCCAGCCCAAGACACACCTTTGAAAAACA 328
QY 280 GAAAAAGATGCCAGGCCCAAGCGGCTGATGTGTCCAAATATCCCTTCGGTTCCGGGAT 339
DB 329 GAAAAAGATGTCAGGCCCAAGCGGCTGATGTGTCCAAATATCCCTTCAGGTTCCGGGAT 388
QY 340 CCAGACCTCGACCAATGTTTGG 362
DB 389 CCGACCTCGACCAATGTTTGG 411

RESULT 7
US-09-864-761-28375
Sequence 28375; Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecm1ca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILLING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILLING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILLING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/532,366
PRIORITY FILLING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILLING DATE: 2000-10-04

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```

Query Match      8.2%; Score 109.6; DB 9; Length 125;
Best Local Similarity 92.7%; Pred. No. 7,4e-21;
Matches 115; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY          239 CGACCGAGCGGCGAGCCGCCAGACACAACCTTGTGAAAAACAGAAAAAAGAATCCAGCCCCA 298
            |||||
Db           1 CGAGGGATGGCCAGGCCCCAGACACACTTCCTGAAAAACAGAAAAACAAGTCTCAGCCCCA 60

QY          299 AGCGGCTGCATGTGTCCCAACATCCCCTTCGSGTTCCGGGAATCCAGACCTCCGACAAATGT 358
            |||||
Db           61 AGCGGCTGCATGTCTCCAATATCCCCTTCAGGTTCCGGGATCCGGACCTCAGACAAATGT 120

QY          359 TTGG 362
            ||||
Db           121 TTGG 124

RESULT 8
US-10-029-386-26339
; Sequence 26339, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

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[illegible]

Query Match	6.7%	Score 90.4;	DB 13;	Length 502;
Best Local Similarity	82.5%	Pred. No. 4.7e-15;		
Matches 188; Conservative	0;	Mismatches 31;	Indels 9;	Gaps 7

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QY 1 GCGCGCGCCCTGACACATGCTCAG-CTTATGCTCAGCGAGTTGCTCCACCCGAG 59
Db 134 GCGCGCGCCCTGACACATGCTCAG-CTTATGCTCAGCGAGTTGCTCCACCCGAG 193
QY 60 AATGGCATCTCT-GCAGATACACGCGCCCTCATCCCATCCCGCCGAGG-ACACCGGC 117
Db 194 AATGGCATCTCT-GCAGATACACGCGCCCTCATCCCATCCCGCCGAGG-ACACCGGC 253
QY 118 CACCCCACTGCTCCCG-CCACACATTAACCTTG-ATCTCTCTACACAGACGACTCGAG 175
Db 254 CACACACGCTTCCCGAGCACAATTAACTGTAACCTTCCCGCCGAGGACTCGAG 313
QY 176 CAGAGC---GCTTATACAGCGCAG-CCGTCTCCGCGACCGCCACA 219
Db 314 CAGAGCGCGCGGACAGAGCGCTCAGACCGCTCTCTGGACCGCCACA 361

RESULT 10
US-09-864-761-22653
; Sequence 22653, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00673
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; SEQ ID NO 22653
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: MAP TO AC006075.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: NT HIT: g18922072, EVALUE 1.00e-123
; OTHER INFORMATION: SWISSPROT HIT: Q09457, EVALUE 8.00e-03
; OTHER INFORMATION: EST_HUMAN HIT: A0118435.1, EVALUE 1.00e-123
US-09-864-761-22653

Query Match 6.6%; Score 88; DB 9; Length 224;
Best Local Similarity 82.6%; Pred. No. 1,4e-14;
Matches 185; Conservative 0; Mismatches 30; Indels 9; Gaps 7;

QY 5 CCGCCCTGACACATGCTCAG-CTTATGCTCAGCGAGTTGCTCCACCCGAGATG 63
Db 1 CTGCCCCCTACACATGCTCAGCTTACGCTTCCGCCAGTTGCTCCCGCGAGAG 60
QY 64 GCATCTCT-GCAGATACACGCGCCCTCATCCCATCCCGCGCAGAG-ACACCGCCAGC 121
Db 61 GATCCCCCGGAAATACAGCGCCCTCATCCCATCCCGCGCAGAGTACAGAGCCAGAG 120
QY 122 CCAGTGTCCCG-CCACACATTAACCTTG-ATCTCTCTACACAGACGACTCGAGCAGA 179
Db 121 CCACGCTTCCCGAGCACAATTAACTGTACTCTCCCGCCGAGCAGCACTCCGAGCAGA 180
QY 180 GC---GCTTATACAGCGCAG-CCGTCTCCGCGACCGCCACA 219
Db 181 GCGCGCGGACAGAGCGCTCAGACCGCTCTCTGGACCGCCACA 224

RESULT 11
US-09-864-761-5893
; Sequence 5893, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 5893
LENGTH: 454
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006075.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
US-09-864-761-5893

Query Match 6.4%; Score 86.4; DB 9; Length 454;
Best Local Similarity 83.5%; Pred. No. 6e-14;
Matches 157; Conservative 0; Mismatches 26; Indels 5; Gaps 5;

QY 1 GCGGCGCGCCCTGACACATGGCTCAG-CTTATGCTCTCAGCGCAGTTGCTCCACCCGAG 59
DB 246 GCGGCTGCTCCCTGACACATGGCTCAGCTTACGCTTGCGCCGAGTTGCTCCCGCCGAG 305
QY 60 AATGGCATCTCT-GGAGAAATACACGCGCCCTCATCCCATCCCGCGCCAGAG-ACACGGGC 117
DB 306 AACGGTATCCCCGGGGAATACACGCGCCCTCATCCCATCCCGCGCCAGAGTACACAGAG 365
QY 118 CAGCGCACTGTCCCGG-CCACACATTAACCTTG-ATCCTCTTACACAGAGCGACTCGGAG 175
DB 366 CAGACCAAGGTTCCCGGACACACATTAACCTGTACCTCCCGCCGAGGCACTCCGAG 425
QY 176 CAGAGCGC 183
DB 426 CAGAGCCC 433

RESULT 12
US-10-292-798-1837/c
Sequence 1837, Application US/10292798
Publication No. US2003023583A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABRATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1837
LENGTH: 2350

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE:
LOCATION: (1)..(2350)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2150)
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)..(2)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (7)..(7)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (9)..(9)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (13)..(15)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (17)..(18)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (20)..(21)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (23)..(24)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (31)..(31)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (34)..(34)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (39)..(39)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (41)..(41)
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FEATURE:
NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified_base
LOCATION: (51)..(51)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (71)..(71)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (73)..(73)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (77)..(77)
OTHER INFORMATION: a, t, c, g, unknown or other

:	FEATURES:
:	NAME/KEY: modified base
:	LOCATION: (85)..(85)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (90)..(90)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (92)..(93)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (95)..(95)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (99)..(100)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (103)..(103)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (106)..(106)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (109)..(109)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (111)..(111)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (113)..(113)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (170)..(171)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (179)..(179)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (195)..(195)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (197)..(197)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (209)..(209)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (212)..(212)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (214)..(214)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:
:	NAME/KEY: modified base
:	LOCATION: (216)..(216)
:	OTHER INFORMATION: a, t, c, g, unknown or other
:	FEATURE:

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1 NAME/KEY: modified base
2 LOCATION: (218) ..(218)
3 OTHER INFORMATION: a, t, c, g, unknown or other
4
5 FEATURE:
6 NAME/KEY: modified base
7 LOCATION: (290) ..(291)
8 OTHER INFORMATION: a, t, c, g, unknown or other
9
10 FEATURE:
11 NAME/KEY: modified base
12 LOCATION: (302) ..(302)
13 OTHER INFORMATION: a, t, c, g, unknown or other
14
15 FEATURE:
16 NAME/KEY: modified base
17 LOCATION: (309) ..(309)
18 OTHER INFORMATION: a, t, c, g, unknown or other
19
20 FEATURE:
21 NAME/KEY: modified base
22 LOCATION: (315) ..(315)
23 OTHER INFORMATION: a, t, c, g, unknown or other
24
25 FEATURE:
26 NAME/KEY: modified base
27 LOCATION: (317) ..(317)
28 OTHER INFORMATION: a, t, c, g, unknown or other
29
30 FEATURE:
31 NAME/KEY: modified base
32 LOCATION: (320) ..(320)
33 OTHER INFORMATION: a, t, c, g, unknown or other
34
35 FEATURE:
36 NAME/KEY: modified base
37 LOCATION: (323) ..(323)
38 OTHER INFORMATION: a, t, c, g, unknown or other
39
40 FEATURE:
41 NAME/KEY: modified base
42 LOCATION: (327) ..(327)
43 OTHER INFORMATION: a, t, c, g, unknown or other

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Query Match	4.3%	Score 58	DB 12	length 2350
Best Local Similarity	57.5%	Pred. No.	1.8e-05	
Matches 103	Conservative	0	Mismatches 76	Indels 0
				Gaps 0

[illegible]

RESULT 13
 US-10-017-161-2191/c
 Application 2191. Application US/10017161
 Publication No. US20030143668A1
 GENERAL INFORMATION:
 APPLICANT: SUMA, MAKITO
 APPLICANT: ASAI, KIYOSHI
 APPLICANT: AKUTAMA, YUTAKA
 APPLICANT: ABURATANI, HIROYUKI
 TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 084335/0152
 CURRENT APPLICATION NUMBER: US/10/017,161
 CURRENT FILING DATE: 2002-12-18
 PRIOR APPLICATION NUMBER: JP 2001/246789
 PRIOR FILING DATE: 2001-06-18
 NUMBER OF SEQ ID NOS: 2430
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 2191
 LENGTH: 2350
 TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(2350)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2150)
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (7)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (9)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (13)..(15)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (17)..(18)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (20)..(21)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (23)..(24)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (31)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (34)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (39)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (41)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (49)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (51)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (71)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (73)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (77)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base

LOCATION: (85)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (90)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (92)..(93)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (95)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (99)..(100)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (103)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (106)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (109)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (111)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (113)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (170)..(171)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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LOCATION: (179)
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FEATURE:
NAME/KEY: modified_base
LOCATION: (195)
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NAME/KEY: modified_base
LOCATION: (197)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (209)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (212)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (214)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (216)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (218)

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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (290)..(291)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (302)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (309)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (315)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (317)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (320)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (323)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (327)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (332)

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: January 15, 2004, 06:08:59 ; Search time 105 Seconds
(without alignments)
5632.889 Million cell updates/sec

Title: US-09-809-545A-1
Perfect score: 1340
Sequence: 1 GCGGCGCGCCGACACACAT.....GGCGGAGGCGTCTGCTAGA 1340

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents NA: *
2: /cgn2_6/prodata/2/ina/5A COMB. seq: *
3: /cgn2_6/prodata/2/ina/5B COMB. seq: *
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5: /cgn2_6/prodata/2/ina/6B COMB. seq: *
6: /cgn2_6/prodata/2/ina/PCTUS COMB. seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	857.2	64.0	2372	3 US-09-145-391-1	Sequence 1, Appl
2	275.6	20.6	1506	3 US-09-176-657-5	Sequence 5, Appl
3	275.6	20.6	1506	4 US-09-421-299-5	Sequence 5, Appl
4	51.4	3.8	2447	2 US-09-014-969-14	Sequence 14, Appl
5	50	3.7	7218	1 US-08-232-463-14	Sequence 6, Appl
6	49	3.7	240	1 US-08-628-417-6	Sequence 1, Appl
7	48	3.6	1696	4 US-09-835-811-1	Sequence 3, Appl
8	45.2	3.4	1338	3 US-09-027-064-3	Sequence 1, Appl
9	45.2	3.4	1338	3 US-09-271-815-3	Sequence 1, Appl
10	45.2	3.4	2394	3 US-09-027-064-1	Sequence 1, Appl
11	45.2	3.4	2394	3 US-09-271-815-1	Sequence 1, Appl
12	45	3.4	2277	1 US-08-676-867-2	Sequence 2, Appl
13	45	3.4	2277	1 US-08-676-867-2	Sequence 2, Appl
14	45	3.4	2277	1 US-08-676-867-2	Sequence 2, Appl
15	44.8	3.3	1477	4 US-09-098-487-2	Sequence 1019, Ap
16	44.8	3.3	1477	4 US-09-620-312D-1019	Sequence 1019, Ap
17	44.8	3.3	1995	4 US-09-620-312D-908	Sequence 908, Appl
18	44.8	3.3	1995	4 US-09-620-312D-908	Sequence 908, Appl
19	42.4	3.2	7286	3 US-09-331-581-3	Sequence 3, Appl
20	42.4	3.2	7286	3 US-09-331-581-3	Sequence 3, Appl
21	42.2	3.1	3994	4 US-09-331-581-14	Sequence 14, Appl
22	42.2	3.1	3994	4 US-09-331-581-14	Sequence 14, Appl
23	42.2	3.1	3994	4 US-09-331-581-14	Sequence 14, Appl
24	42.2	3.1	3994	4 US-09-331-581-14	Sequence 14, Appl
25	42.2	3.1	3994	4 US-09-331-581-14	Sequence 14, Appl
26	41.4	3.1	6243	2 US-09-056-075-1	Sequence 1, Appl
27	41.4	3.1	2026	2 US-08-993-228-3	Sequence 3, Appl

28	40	3.0	80246	3 US-09-078-294-4	Sequence 4, Appl
29	40	3.0	80595	3 US-09-078-294-3	Sequence 3, Appl
30	39.8	3.0	370	2 US-08-332-766A-8	Sequence 8, Appl
31	39.8	3.0	1069	4 US-09-372-422A-7	Sequence 7, Appl
32	39.6	3.0	227	2 US-08-520-678A-28	Sequence 28, Appl
33	39.6	3.0	227	3 US-08-897-126-28	Sequence 28, Appl
34	39.6	3.0	1781	4 US-08-818-512-1	Sequence 1, Appl
35	39.6	3.0	2621	2 US-08-553-619B-8	Sequence 8, Appl
36	39.4	2.9	263	4 US-09-091-097-26	Sequence 26, Appl
37	39.4	2.9	976	2 US-08-504-459-9	Sequence 9, Appl
38	39.4	2.9	2908	4 US-09-904-615-35	Sequence 35, Appl
39	39.2	2.9	1065	4 US-08-765-907A-7	Sequence 7, Appl
40	39.2	2.9	1545	4 US-09-559-023-1	Sequence 1, Appl
41	39.2	2.9	1737	1 US-08-202-056-4	Sequence 4, Appl
42	39.2	2.9	1737	1 US-08-076-093A-3	Sequence 3, Appl
43	39.2	2.9	1737	1 US-08-701-265-3	Sequence 3, Appl
44	39.2	2.9	1737	1 US-08-284-586-3	Sequence 3, Appl
45	39.2	2.9	1737	2 US-08-805-478-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-145-391-1
Sequence 1, Application US/09145391
Patent No. 6194171

GENERAL INFORMATION:
APPLICANT: Pulset, Stefan M.
APPLICANT: Shibata, Hiroki

TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
TITLE OF INVENTION: Products Related Thereto and Methods of Using Same

FILE REFERENCE: CE 3093

CURRENT FILING DATE: 1998-09-01

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 1

LENGTH: 2372

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (987) .. (1979)

US-09-145-391-1

Query Match

Best Local Similarity 82.7%; Pred. No. 3.4e-234;

Matches 1141; Conservative 0; Mismatches 138; Indels 101; Gaps 10;

QY	1	GGGCGCGCCCGGACACATGCTCAG-CTTATGCTCAGCGCAGTTCGCTCCACCCGAG	59
DB	1029	GGCGTGGCCCTGACACATGCTCAGCTTACGCTTCGCGCCAGTTCTCCCGCGAG	1088
QY	60	AATGATCTCT-GCAGATATACAGCGCCCTCATCCCATCCGCGCCAGAG-ACACCGGC	117
DB	1089	AACGATATCCCGCGGAAATACAGCGCCCTCATCCCATCCGCGCGACAGTACAGGC	1148
QY	118	CAGCCCATCTGCTCCCG-CCACACATTAACCTTG-ATCTCTCTACACAGCGCATCTCGAG	175
DB	1149	CAGACACAGCTTCCGAGACACATTAACCTTGATCCCTCCGCGCCAGCGCATCTCGAG	1208
QY	176	CAGAGC---GCTTATACAGCGACAG-CCGCTCCGCGACCGCCACAGCAGATGAT	231
DB	1209	CAGAGCGCGCGGACACAGCGCTCAGACCGTCTCTGCGACCGCCACAGCAGATGAC	1268
QY	232	GGCGCCCGGACCGGACCGCGCCAGCCAGACACACCTTCTGAAAACAGAAAAACAAGTCC	291
DB	1269	GGAGCAGCGAGGATGGCGCCAGCCAGACACACCTTCTGAAAACAGAAAAACAAGTCT	1328
QY	292	CAGCCCAAGCGGCTGATGTCTCAACATCCCTTCGCTTCGCGGATTCAGACCTCCGA	351
DB	1329	CAGCCCAAGCGGCTGATGTCTCAACATCCCTTCGCTTCGCGGATTCGAGACCTCCGA	1388

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QY 352 CAATGTTGGCCAAATTTGGTAAATATAGATGTTGAATTTATTTTAAATGACGGGCG 411
DB 1389 CAATGTTGGTCAATTTGGTAAATTTAGATGTTGAATTTATTTTAAATGACGGGCG 1448
QY 412 TCGAAGGAAATTTGTTTCTGTAATCTTTCGAAATATGTCGGATGCGACAGGGGAGGAG 471
DB 1449 TCAAGGAAATTTGTTTCTGTAATCTTTCGAAATATGTCGGATGCGACAGGGGAGGAG 1508
QY 472 AAATTCAGGTAATCCGTTGTAAGAGGGCGGTAATGAGGTTATATATGACAGCAGCG 531
DB 1509 AAATTCAGGTAATCCGTTGTAAGAGGGCGGTAATGAGGTTATATATGACAGCAGCG 1568
QY 532 GTGATGCTAATATATATATATATATATATATATATATATATATATATATATATAT 591
DB 1569 GTATATGCAATATATATATATATATATATATATATATATATATATATATATATAT 1628
QY 592 GTGGGCGCGGCTTACAGCCCGGACTTCTATGACAGCAGGTCGTGTGTGCGCAGGCCAC 651
DB 1629 GTGGGCTGCACTTACAGTCCCGAATCTATGACAGCAGGTCGTGTGTGCGCAGGCCAC 1688
QY 652 CAGAGGGAATCTTCCATGTAAGTGGCCGAGTTCACTTGTATATATATATATATATAT 711
DB 1689 CAGAGGGAATCTTCCATGTAAGTGGCCGAGTTCACTTGTATATATATATATATATAT 1748
QY 712 GGGCTTTCATATCCGGCGGCGCACTGTGACAGTGCATACCGAGGGGCTCACTTCAGAGG 771
DB 1749 GGGCTTTCATATCCAGAGGCGCACCGCGCGGCTTACCGAGGGGCGCACCTGCGAGGCG 1808
QY 772 CGTGTGCGACCGGTGACCAACCTTTCAGAGTGGCGGCGGCGGCGGCGGCGGCGGCGG 831
DB 1809 CGGCGGTGCGACCGGTGACCAACCTTTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1868
QY 832 TAATGGCGAATAGTATCAAGAGCCAGTGTATGCGAATTAATGTCTACAGGGGTGTAC 891
DB 1869 TAAGGCGGTGTGTATAC--CAGATGATTTATGTGTGCGACATTTATGTGTAT 1926
QY 892 GGTGCAATACCGCTACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 944
DB 1927 GGTGCAATACCGCTACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1986
QY 945 -----CAGTTACGAGCAG 958
DB 1987 CAGTTGCTTCTGTTGACAGATGAATTTCTGTAAACACTTCTGCAAGTTACGAGCAG 2046
QY 959 TTTATGCTGCGGACCCCTTACACACACACTTGTCTCCAGCCCGGCTTACGAGGCTGTG 1018
DB 2047 TTTATGCTGCGGACCCCTTACACACACACTTGTCTCCAGCCCGGCTTACGAGGCTGTG 2106
QY 1019 CCAATGAATGCTTTGCGCCCTTACAGCGATGCAAGACTAGAGGCGATGATGATGTG 1078
DB 2107 CCAATGAATGCTTTGCGCCCTTACAGCGATGCAAGACTAGAGGCGATGATGATGTG 2166
QY 1079 GTCTGCTTCTTCTTCAATGAGGCTATATATATATATATATATATATATATATATAT 1138
DB 2167 GTCTGCTTCTTCTTCAATGAGGCTATATATATATATATATATATATATATATATAT 2226
QY 1139 CATTTTAAATGATTAACCATTAACCAAGCAAAAAACAAAAACAAAAAAC 1198
DB 2227 CATTTTAAATGATTAACCATTAACCAAGCAAAAAACAAAAACAAAAAAC 2250
QY 1199 CAACCTTCCATGTTGGGAGAGAGAAAGCTTTCGAGGCGCGAGTGTGCGACATGCA 1258
DB 2251 -AACCTTCCATGTTGGGAGAGAGAAAGCTTTCGAGGCGCGAGTGTGCGACATGCA 2309
QY 1259 GTAGGACATCACTTTAGCAACTCAAGAAACCAAGAAAAAATTTTAAATTTAA 1318
DB 2310 GTAGGACATCACTTTAGCAACTTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2369

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RESULT 2
US-09-176-657-5
; Sequence 5, Application US/09176657

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; Patent No. 6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176,657
; CURRENT FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 1250374
US-09-176-657-5

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Query Match: 20 6%; Score 275.6; DB 3; Length 1506;
Best Local Similarity 60.2%; Pred. No. 1.5e-68;
Matches 601; Conservative 0; Mismatches 354; Indels 43; Gaps 7;
QY 222 GACAGATGATGCGCGCCCGACCGACGCGCGCAGC---CCAGACACAACCTTCTGAAAAAC 278
DB 452 GACAGAAAGTGTGAGACACAGACAGACCGCGCAGAGTACAGACACAAGTGTGAAATTC 511
QY 279 AGAAAAAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 338
DB 512 AGAGATTAATCTAACCCCGAAACGCGTGCATGTCTTAATATCTTTCGCTCCGCGGA 571
QY 339 TCCAGACCTCCGCAATATGTTGGCCATTTGGTAAATATATATATATATATATATAT 398
DB 572 CCTGACCTCCGCAATATGTTGGCGAGTGTGCAAAATCTTGAATGAATTAATCTT 631
QY 399 TAATGACGCGGCGCTGAAAGGATTTGTTCTGTAATCTTGAATATATGTCGATGCGGA 458
DB 632 TAATGACGCGGCTTAAAGGATTTGCGGTTCTGTAATCTTGAATATATGTCGATGCGGA 691
QY 279 AGAAAAAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 338
DB 512 AGAGATTAATCTAACCCCGAAACGCGTGCATGTCTTAATATCTTTCGCTCCGCGGA 571
QY 339 TCCAGACCTCCGCAATATGTTGGCCATTTGGTAAATATATATATATATATATATAT 398
DB 572 CCTGACCTCCGCAATATGTTGGCGAGTGTGCAAAATCTTGAATGAATTAATCTT 631
QY 399 TAATGACGCGGCGCTGAAAGGATTTGTTCTGTAATCTTGAATATATGTCGATGCGGA 458
DB 632 TAATGACGCGGCTTAAAGGATTTGCGGTTCTGTAATCTTGAATATATGTCGATGCGGA 691
QY 459 CAGGCGGAGGAGAAATTTGACCGGTACCGTGTAGAGGCGCGTAAATGAGGTTAATA 518
DB 692 CAGGCGGAGGAGAAATTTGACCGGACCGGTGTAGAGGCGCGTAAATGAGGTTAATA 751
QY 519 TGGGACAGCAGCGGTATGACTAATATATATATATATATATATATATATATATAT 578
DB 752 TGGTACAGCAGCGGTATGACTAATATATATATATATATATATATATATATATAT 811
QY 579 ATTAATATCAGTTGTGGGCGCGGTCTACAGCCCGGACTTCTATGACG-----GCA 628
DB 812 ATTAATATCAGTTGTGGGCGCGGTCTATATATATATATATATATATATATATATAT 871
QY 629 CGGTGCTGTGTGCGACGCGGACAGAGGAGATCTTCATGTA--CAGTGGCCCGAGTTC 686
DB 872 AGCAGATGTGTCTTACGCAATGATGACAGGAGGCGGCTTACAGAAAGAGGAGGATCA 931
QY 687 ACTTGTATATATCTTGTGCAATGCTGCTTCCATA--TCGGGCGCGCACTGCTGAGC 743
DB 932 CACTTACATTCCTTATATATATATATATATATATATATATATATATATATATATAT 991
QY 744 TGCATACGAGGAGGCTACCTTCAAGGCGGTGTGCGACCGGTATACAACTTCAAGGC 803
DB 992 CGCTTTTACAGAGGCCATTTTGAAGGCGAGAGGCGGACAGTATATATGTCGATGCGGA 1049
QY 804 TGGCGGCGGCGGACCGGCAATTCGCGCTATATGCGGAGTATGATATCAAGCCAGTGT 863
DB 1050 -GGGTACTCTCAACAGCCATCCCGGCTATCCAGGGGTGATATGACGCTACAG----- 1104
QY 864 TGGCAATTAATTTGCTACAGGAGTGTATACGTGATACCGGTACGCGCCAGCCACCCCTGC 923
DB 1105 -----ATATGACAGCGCTGTACTGTACCAACGCGACGCGCGCTGTGAGC 1149

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QY	924	CACGCGCTGCTCCATACAGTGAAGTTACGAGACGAGTTATCTGGCCGACCCCTACACACA	983
Db	1150	CGCTGCACGCCCTTACAGTGAACGTTAAGCAGGGGTGACACAGCCGACCCCTACACATGC	1209
QY	984	CACACTTGCTCCAGGCCCCACCTACGCGCGTTGGTGCATGAATGCTTTTGGCGCCTTGCAC	1043
Db	1210	C---CTTGGCCCTCCGCTACCTATGAGTTGGCGCTGTGCAGATTATATCCAGGTGG	1266
QY	1044	CGATGCCAAGCTACGAGCCGATGCTGAATGATGTGGGTCTCGTTCTTTCTTCAATGCAGGC	1103
Db	1267	CTACAGCCGATTTTGCCCCCTTACTGAAGTGAAGTGAACCCCTGCATAATGGACACGCCCC	1328
QY	1104	TAGTATATATCAAGAGGGGATACAACCGTTTTGCTTCATATTTAAATGATAAACCATTA	1163
Db	1327	CAGTTTCATGAGGCCCTGCGCTATTTGCATATTTACTAGTGAAGAACTATATGCAAGATGA	1386
QY	1164	CAACCAAGCAAAAAACAACAAAAACAACAAAAACAACAAAAACAACAAAAACAACAAAAACA	1201
Db	1387	AGAGAAAAACAACAAAAACAACAAAAACAACAAAAACAACAAAAACAACAAAAACAACAAAA	1424

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RESULT 3
US-09-421-299-5
: Sequence 5, Application US/09421299
: Patent No. 6524579
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Lu, Aina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PR-0611 US
: CURRENT APPLICATION NUMBER: US/09/421,299
: CURRENT FILING DATE: 1999-10-20
: EARLIER APPLICATION NUMBER: 09/176,657
: EARLIER FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: -
: OTHER INFORMATION: 1250374
: US-09-421-299-5

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Query Match	20.6%	Score 275.6	DB 4	Length 1506
Best local Similarity	60.2%	Pred. No. 1.5e-68		
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QY	222	GACGATGATGTCGGCCCGACCGAGCGCCAGC	---	CCGACACACACTTTGTGAAACAC 278
Db	452	GACGAAAGGTGAGACACAGACAGACGGCAGACAGTACACAGACACAAAGTGTGAAATTC		511
QY	279	AGAAACAAAGTCCGAGCCCAAGCGGCTCATGTGTCCAACATCCCGCTCCGGTCCGGGA		338
Db	512	AGAGAGTAAATCTTACCCGAAACGGCTGCATGTCTTAAATTTCCCTTCGCGCTCCGGGA		571
QY	339	TCCGAGACTCCGACAAATGTTTGGCCAAATTTGTGTAATATTAGATGTTGAAATTATTTT		398
Db	572	CCCGAGCCTCGGAGAGATGTTTGGCAGATTTGGCAAAATCCTAGATGTAAGAAATATCTT		631
QY	399	TAAAGCGCGGCTCGAAGGATTTGGTTTGTAATCTTCGAAATATAGTGGCATGCCGA		458
Db	632	TAAAGAAAGTGGCTTAAGGATTTGGGTTGTAACTTTCGAAATATAGTCGATGCAGA		691
QY	459	CAGGCGGAGGAGAAATTGCACGATCCTGTGTAAAGGCCGTAAATTCGAGTTAAATA		518
Db	692	CAGGCGCAGGAGAAATTACACGCAACCTGTGTAAAGGCCGTAAATTCGAGTTAAATA		751

QY	519	TGGCAGCAGCAGCGGTATGCTATATATAAAAGGCGGTGAACCCCTACACCAATGGCTGGAA	578
Db	752	TGCTACAGCAGCGGTATATGCACTAATGAAAGATGTCACACCAATGTGCAATGGTTGGAA	811
QY	579	ATTAAATCCAGTGTGTGGCGCGGTCTACAGCCCCGACTTCTATGACG-----GCA	628
Db	812	ATTAAAGCCAGTATGTTGAGCTGTATATGTGTCGGAGATTATATGACATTCAGCTTTCA	871
QY	629	CGGTGCTGTGTGTCAGAGCCCAACAGAGGGAATCTTCATGTA--CAGTGGCCCCAGTTC	686
Db	872	AGCAGATGTGTCCTTAGGCAATATGACAGCATGTCCTCTATCAGAAAGAGGGGTATCAAA	931
QY	687	ACTGTATATATCTTCTGCATATGCTGTGCTTTCCATA---TCGGCGCGCACTGTGTGAGC	743
Db	932	CACCTACATTCCTTTATATCATATCTGTGCTTCCCTTACCTTACGTGACCCACACAGGCAAGC	991
QY	744	TGCATACCGAGGGAGTCACTTCAGAGGCGGTGTGTCGACCGGTGTAACAACCTTCAGAGC	803
Db	992	CGCTTTACAGAGAGCCCATTTTGAAGGGCAGAGGGCGGACAGTATATGTGTCAAGTCCGA--	1049
QY	804	TGCGGCGCCCCCAACCCCAATCCCGGCTTATGGCGAGTAGTAGTATCAAGAGCCAGTGA	863
Db	1050	-GGGTATCTTCAACAGCATTCCCGGCTTATCCAGGGGGTGAATATGACGCTACAG----	1104
QY	864	TGGCATTAATATGCTACAGGGGTGTTACGCTGCATACCGCTGAGGCCAGCCACCTCTGC	923
Db	1105	-----ATATCACAAGCCTGTCTATCTGCACACGCAACCCAGCTGTGTGAGC	1149
QY	924	CACGTGCTGCTGCTTACAGTGACAGTTAACGAGACAGTTTATGCTGCCAGCCCTTACACGA	983
Db	1150	CGCTGACGCGCTTACAGTACGGTTATGCGAGGGTATACACAGCCGACCCCTTACCATGC	1209
QY	984	CACACTTGTCTCAGACCCCACTACGCGCGTTGTGTGCATGAATGCTTTTGGCGCCCTTGAC	1043
Db	1210	C-----CTTGGCCCTGCGCGCTATGCTATGGAAGTTGGGGCTGTGGCAGATTATACGAGGTGG	1266
QY	1044	CGATGCCAAGACTAGAGAGCCATGCTATGATGTGTGGTCTTCGTTCTTTCTTCATTTGAGGC	1103
Db	1267	CTTACAGCCGATTTTGCCCTTACGTAAGTGAACGTGAGACCCCTGCAAAATGGGACAGCCCC	1326
QY	1104	TAGTATATACCAAGGGGATACACCGTTTGTCTCCATATTAATGATATAAACCATTTAA	1163
Db	1327	CAGTTCATGAGGCTGTGCTATTGCAATATTTACTATGTAAGGAACCTTATAGCAAGATGA	1386
QY	1164	CAAAACAAGCAAAAAACAAACCAAAAAACCAAAAAACCA	1201
Db	1387	AGAGAAAAACAAACAAACAAACAAACAAACAAACAAACAA	1424

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1      RESULT 4
2      US-09-014-969-14
3      : Sequence 14, Application US/09014969
4      : Patent No. 5965397
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Jacobs, Kenneth
9      : APPLICANT: McCoy, John M.
10     : APPLICANT: Lavallee, Edward R.
11     : APPLICANT: Racie, Lisa A.
12     : APPLICANT: Merberg, David
13     : APPLICANT: Treacy, Maurice
14     : APPLICANT: Spaulding, Vikki
15     : APPLICANT: Agostino, Michael J.
16     : TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
17     : TITLE OF INVENTION: ENCODING THEM
18     :
19     : NUMBER OF SEQUENCES: 32
20     :
21     : CORRESPONDENCE ADDRESS:
22     : ADDRESSEE: Genetics Institute, Inc.
23     : STREET: 87 CambridgePark Drive
24     : CITY: Cambridge
25     : STATE: MA
26     : COUNTRY: U.S.A.
27     : ZIP: 02140
28     :
29     : COMPUTER READABLE FORM:
30     :

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-014-969-14

Query Match 3.8%; Score 51.4; DB 2; Length 2447;
Best Local Similarity 52.1%; Pred. No. 0.00015;
Matches 112; Conservative 1; Mismatches 102; Indels 0; Gaps 0;

QY 1104 TAGATATACCAAGGGGATACACCGTTTGTCTCCATATTAATGATTAACCATTA 1163
DB 2209 TTGACTTTAAATGTGCAATTAACCTTTGGAGAAAAAATTAATTAATTA 2268
QY 1164 CAACAACGAAAAAACAACAAAAAACAACCTTCCATGTGGGAGAGAG 1223
DB 2269 AA 2328
QY 1224 AAGCTTCCGAGCCGAGTGTTCGACATGATGATGACATCTTAAGCACTCA 1283
DB 2329 AA 2388
QY 1284 AGAACAACGAAAAAACAACAAAAAACAACCTTCCATGTGGGAGAGAG 1318
DB 2389 AA 2423

RESULT 5

US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F18
US-08-232-463-14

Query Match 3.7%; Score 50; DB 1; Length 7218;
Best Local Similarity 7.5%; Pred. No. 0.0007;
Matches 17; Conservative 132; Mismatches 77; Indels 0; Gaps 0;

QY 1106 GTTATACCAAGGGGATACACCGTTTGTCTCCATATTAATGATTAACCATTA 1165
DB 1467 GCAAGTAGTTAAAGATGAAAGAAATTTGTACRRRRRRRRRRRRRRRRRR 1408
QY 1166 AACAGCAAAAAACAACAAAAAACAACCTTCAATGTGGGAGAGAGAA 1225
DB 1407 RRR 1348
QY 1226 GCTTCCGAGCCGAGTGTTCGACATGACGTAGACATCATCTTAAGCAACTCAAG 1285
DB 1347 RRR 1288
QY 1286 AACAACGAAAAAACAACAAAAAACAACCTTCCATGTGGGAGAGAG 1331
DB 1287 RRR 1242

RESULT 6

US-08-628-417-6
Sequence 6, Application US/08628417
Patent No. 5627054
GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
STATE: MARYLAND
COUNTRY: USA
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 398-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158

TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligodeoxynucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-628-417-6

Query Match 3.7%; Score 49; DB 1; Length 240;
Best Local Similarity 53.4%; Pred. No. 0.00019;
Matches 103; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1126 AACCGTTTCTCCATTTAAATGATTAACCACTTAACCAACAGCAAAACAAACAA 1185
DB 28 AATTAATTTTACTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 87
QY 1186 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 1245
DB 88 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 147
QY 1246 TCGGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 1305
DB 148 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 207
QY 1306 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 1318
DB 208 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 220

RESULT 7
US-09-835-811-1
; Sequence 1, Application US/09835811
; Patent No. 6482936
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL0012228
; CURRENT APPLICATION NUMBER: US/09/835,811
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
US-09-835-811-1

Query Match 3.6%; Score 48; DB 4; Length 1696;
Best Local Similarity 53.1%; Pred. No. 0.0011;
Matches 102; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1127 ACCGTTTCTCCATTTAAATGATTAACCACTTAACCAACAGCAAAACAAACAA 1186
DB 1502 ACTGATAGATTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 1561
QY 1187 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 1246
DB 1562 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 1621
QY 1247 GCGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 1306
DB 1622 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 1681
QY 1307 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 1318
DB 1682 AAAAAAATTTTAACTTTCAATGTGGGAGAGAGAACTTTCCGAGCCCGAGTGT 1693

RESULT 8
US-09-027-064-3
; Sequence 3, Application US/09027064
; Patent No. 6133006
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: BERGSMAN, DERR
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 20-FEB-1998
; APPLICATION NUMBER: US/09/027,064
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,924
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1338 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-027-064-3

Query Match 3.4%; Score 45.2; DB 3; Length 1338;
Best Local Similarity 47.8%; Pred. No. 0.0062;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGGCGCCCTGACACATGAGCTGACCTATGCTTACAGCGCACTTGGCTCCACCCAGAT 62
DB 686 GGTCTGCTCCCATCACCACCCCTTACCCACCCCGAGAGTATGATGTGAGCTGTG 745
QY 63 GGCATCTGTCAGATACAGAGCGCCCTTATCCCATTCGCGGAGAGACCGGCGAGCC 122
DB 746 GGGCGCTGCTCTACCTCTCCCATCTTACAGCGCTTCCCGGAGAGACCGGCGAGCC 805
QY 123 CACTGCTCCCGACACATTAATTTGATCTCTTACACAGACGCACTGAGACAGAGCG 182
DB 806 CAGCCCTCGGAGCTGAGATGATGAGAGGTGTCTCACCCCTCCGCTCTGATGACCTG 865
QY 183 CTATATCAAGCCGACAGCGCTCTCCGAGCGCCGACACAGACAGATGATGAGCGCCGAGC 242
DB 866 CCACTCTGGGCTTACCTCTGAGTGTACCTCCAGAGACAGACAGCAAGCTGTG 925
QY 243 CGAGCGCAGCCCGACACATCTTCTGAATC 276
DB 926 ACCCTGCCCCCTCTCTGGGCGCCCTCTCTGAAGC 959

RESULT 9

US-09-271-815-3
Sequence 3, Application US/09271815
Patent No. 6297036
GENERAL INFORMATION:
APPLICANT: BERGSMAN, DERK
TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
FILE REFERENCE: GH-70172-1
CURRENT FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: 09/027, 064
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 60/053, 924
EARLIER FILING DATE: 1997-07-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1338
TYPE: DNA
ORGANISM: Homo sapiens
US-09-271-815-3

Query Match 3.4%; Score 45.2; DB 3; Length 1338;
Best Local Similarity 47.8%; Pred. No. 0.0062;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGCCGCCCTGACACATGAGCTTATGCTCAGCGCAGTTGCTCCACCCAGAAAT 62
DB 686 GGTGTCTCCATCACCACCTCACCACACCCCGAGCTGATGATGAGCTGTGTG 745
QY 63 GGATCTGTCAGATACAGCGCCCTGATCCCATCCCGCGCAGAGACACCGGCGAGCC 122
DB 746 GCGCGCTGCTGACTGCTGCCACCTCACCAGCGCTGCGCCCGCAGACACCGGCTGCT 805
QY 123 CACTGTCCCGCCGACACATTTAACTTATCTCTTAACAGACGCACTCGGAGAGAGCG 182
DB 123 CACTGTCCCGCCGACACATTTAACTTATCTCTTAACAGACGCACTCGGAGAGAGCG 182
QY 806 CAGCCCTCGGAGCTGAGTGTGAGAGTGTCTTCCACCTCTCCCTGATGATGACCTGT 865
DB 183 CTTATACAGAGCGACAGCGCTCTCCGACCGCCACAGACAGATGATGCGCCCGAC 242
QY 866 CCACTGTGGGAGCTCAGCTGCTCCGCTGCTGATGATGATGATGATGATGATGATG 925
DB 866 CCACTGTGGGAGCTCAGCTGCTCCGCTGCTGATGATGATGATGATGATGATGATG 925
QY 243 CGACGGCCAGCGCCGACACACACCTTGTGAAG 276
DB 926 ACCCTGCCCCCTCTCTGAGGAGCCCTCTGAAAGC 959

RESULT 10
US-09-027-064-1

Sequence 1, Application US/09027064
Patent No. 6133006
GENERAL INFORMATION:
APPLICANT: SHABON, USMAN
TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASE-HTLAR33
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAITNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027, 064
FILING DATE: 20-FEB-1998
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/053, 924
FILING DATE: 28-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23, 031
REFERENCE/DOCKET NUMBER: GH-70172
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-027-064-1

Query Match 3.4%; Score 45.2; DB 3; Length 2394;
Best Local Similarity 47.8%; Pred. No. 0.0087;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGCCGCCCTGACACATGAGCTTATGCTCAGCGCAGTTGCTCCACCCAGAAAT 62
DB 1742 GGTGTCTCCATCACCACCTCACCACACCCCGAGCTGATGATGAGCTGTGTG 1801
QY 63 GGATCTGTCAGATACAGCGCCCTGATCCCATCCCGCGCAGAGACACCGGCGAGCC 122
DB 1802 GCGCGCTGCTGACTGCTGCCACCTCACCAGCGCTGCGCCCGCAGACACCGGCTGCT 1861
QY 123 CACTGTCCCGCCGACACATTTAACTTATCTCTTAACAGACGCACTCGGAGAGAGCG 182
DB 1862 CAGCCCTCGGAGCTGAGTGTGAGAGTGTCTTCCACCTCTCCGCTGATGATGATGATG 1921
QY 183 CTTATACAGAGCGACAGCGCTCTCCGACCGCCACAGACAGATGATGCGCCCGAC 242
DB 1922 CCACTGTGGGAGCTCAGCTGCTCCGCTGCTGATGATGATGATGATGATGATGATG 1981
QY 243 CGACGGCCAGCGCCGACACACCTTGTGAAG 276
DB 1982 ACCCTGCCCCCTCTCTGAGGAGCCCTCTGAAAGC 2015

RESULT 11
US-09-271-815-1

Sequence 1, Application US/09271815
Patent No. 6297036
GENERAL INFORMATION:
APPLICANT: BERGSMAN, DERK
TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
FILE REFERENCE: GH-70172-1
CURRENT APPLICATION NUMBER: US/09/271, 815
CURRENT FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: 09/027, 064
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 60/053, 924
EARLIER FILING DATE: 1997-07-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2394
TYPE: DNA
ORGANISM: Homo sapiens
US-09-271-815-1

Query Match 3.4%; Score 45.2; DB 3; Length 2394;
Best Local Similarity 47.8%; Pred. No. 0.0087;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGCCGCCCTGACACATGAGCTTATGCTCAGCGCAGTTGCTCCACCCAGAAAT 62

Db 1742 GGTCTGTCCTCATCAACCAACCTTCAACCAACCCCGAGCTGATGATGAGCTGTG 1801
Qy 63 GGCATCTCGAGATATACAGGCGCCCTCATCCCATCCCGGCGAGAGACAGCGGCGAGCC 122
Db 1802 GGGGGCTGTGCTACTGTCTCCCACTTCACTCAAGCGGCTGCGCCCGAGACCGGCTGCT 1861
Qy 123 CACTGTCCCGCCAGCAATTAACTTGATCTCTCTTACACAGAGCACTCGAGCAGAGCG 182
Db 1862 CAGCCCTCGGAGCTCGGATGATGAGAGTGTCTCAGCCCTCCCGCTCTGATGACCTG 1921
Qy 183 CTATATACAGCGACAGCGCTCTCCGCGACCGCAACAGACAGATGATGCGCCCGGAC 242
Db 1922 CCACTGTGGGGCTCACTGCTGCTGCTGATACCCAGAGAGCAGCGAGCTGTG 1981
Qy 243 CGAGCGCGAGCCCGAGACAGACACTTCTGAAAC 276
Db 1982 ACCCTGCCCCCTCTCTGCGGCGCCCTCTGAAAGC 2015

RESULT 12

US-08-676-967-2
; Sequence 2, Application US/08676967
; Patent No. 5747317
; GENERAL INFORMATION:
; APPLICANT: COLLINS, KATHLEEN
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,967
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-676-967-2

Query Match 3.4%; Score 45; DB 1; Length 2277;
Best Local Similarity 32.4%; Pred. No. 0.0096;
Matches 109; Conservative 46; Mismatches 178; Indels 3; Gaps 1;

Qy 215 CCACACAGACAGATGATGCGCGCCCGACGAGCGCCAGACAGACAACTTCTGAA 274
Db 257 CNAAGARARAGGNAARAAAGAAAYWSNGARTGVCNNAARARAGARCCNAARAGNAARA 316
Qy 275 ACACAGAAAACAAGTCCCGACCGCAAGCGGCTGATGTCTCAATCCCTTCGGTTC 334
Db 317 ARGCNAGATGNGCAGAAARAAARACGNNGNATYNAATHMGNAAYYTNWSNTTYAARTGW 376
Qy 335 GGATCCAGACTCCGACAAATGTTGGCAATTGGTAATAATATTAAGATTGAATTA 394

Db 377 SNGARGAYAYYTNABACNGNTTYGNCARTTYGNGCNGNTYNGARTNAAYATHC 436
Qy 395 TTTTAA---TGAGGGGGCTCGAAGGGATTGGTTGCTACTTTCGAAAATAGCGCG 451
Db 437 CMGNARACNGCAGGNAARATATGNGGNTTYGNTTYGNTTYGNTTYGNTTYGNTTYG 496
Qy 452 ATCCGACAGGGCGAGGGAATTGACAGTACCGTGTAGAGGGCCGTAATAATCGAG 511
Db 497 ARGCNAGNARACNTTNAARGNATGAAYATGAARARATTHARGNMNACNGTNGCNG 556
Qy 512 TTAATATCGACAGACGCGGTGATGATTAATAAA 547
Db 557 TNGAYTGGCGNGTNGCNAARAGAYAAATYAARGAYA 592

RESULT 13

US-08-676-974-2
; Sequence 2, Application US/08676974
; Patent No. 5770422
; GENERAL INFORMATION:
; APPLICANT: COLLINS, KATHLEEN
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,974
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-676-974-2

Query Match 3.4%; Score 45; DB 1; Length 2277;
Best Local Similarity 32.4%; Pred. No. 0.0096;
Matches 109; Conservative 46; Mismatches 178; Indels 3; Gaps 1;

Qy 215 CCACACAGACAGATGATGCGCGCCCGACGAGCGCCAGACAGACAACTTCTGAA 274
Db 257 CNAAGARARAGGNAARAAAGAAAYWSNGARTGVCNNAARARAGARCCNAARAGNAARA 316
Qy 275 ACACAGAAAACAAGTCCCGACCGCAAGCGGCTGATGTCTCAATCCCTTCGGTTC 334
Db 317 ARGCNAGATGNGCAGAAARAAARACGNNGNATYNAATHMGNAAYYTNWSNTTYAARTGW 376
Qy 335 GGATCCAGACTCCGACAAATGTTGGCAATTGGTAATAATATTAAGATTGAATTA 394
Db 377 SNGARGAYAYYTNABACNGNTTYGNCARTTYGNGCNGNTYNGARTNAAYATHC 436
Qy 395 TTTTAA---TGAGGGGGCTCGAAGGGATTGGTTGCTACTTTCGAAAATAGTGGCG 451

Db 437 CNGMNAARCCNAGVGNABATGNGNGNTTYGGNTTYGTCARCTTAATAAAAYTNTNG 496
Qy 452 ATCCGACAGGGCCAGGAGAGAAATTCACCGTACCGGTAGAGGGCCGTAATAATGAGG 511
Db 497 ARGNGGNAARCCNAGVGNABATGNGNGNTTYGGNTTYGTCARCTTAATAAAAYTNTNG 556
Qy 512 TTATAATGCGACGACGCGGTGATGACTAATAAAA 547
Db 557 TNGAYTGGCGNGTNGCNAARGAVAAATTAARAGAYA 592

RESULT 14
US-09-098-487-2
; Sequence 2, Application US/09098487
; Patent No. 5917025
; GENERAL INFORMATION:
; APPLICANT: COLLINS, Kathleen
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,487
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-098-487-2

Query Match 3.4%; Score 45; DB 2; Length 2277;
Best Local Similarity 32.4%; Pred. No. 0.0096;
Matches 109; Conservative 46; Mismatches 178; Indels 3; Gaps 1;

Qy 215 CCAACAGCAGAGATGATCCGCCCGACGCGCCAGCCCAACCACTTCTGAAA 274
Db 257 CNAARGAABARAGNABARAAVBARAAVMSNGARTGCCAARAPAAAGARCNAARGCNAARA 316
Qy 275 ACACAGAAAACAACTCCACGCCCAAGCGCTGATGTGTCCAAACATCCCTCCGGTTC 334
Db 317 ARGNAARAGTNGCAGAYABARABARCGNMGNTYNNATHATMGAAAYTTMNSNTTYAARGYW 376
Qy 335 GGGATCCAGACCTCCGACAAATGTTGGCCAAATTTGTAAATATTAAGATTTGAATTA 394
Db 377 SNGARGAYGAYTTAARACNGTNTTYGCNCARTTYGGNGCNGTNTYNGARGTNAAYATHC 436
Qy 395 TTTTAA---TGAGGGGGCTCGAAGGATTTGTTGCTTAACCTTGGAAAATAGTGGG 451
Db 437 CNGMNAARCCNAGVGNABATGNGNGNTTYGGNTTYGTCARCTTAATAAAAYTNTNG 496
Qy 452 ATCCGACAGGGCCAGGAGAGAAATTCACCGTACCGGTAGAGGGCCGTAATAATGAGG 511

Db 497 ARGNGGNAARCCNAGVGNABATGNGNGNTTYGGNTTYGTCARCTTAATAAAAYTNTNG 556
Qy 512 TTATAATGCGACGACGCGGTGATGACTAATAAAA 547
Db 557 TNGAYTGGCGNGTNGCNAARGAVAAATTAARAGAYA 592

RESULT 15
US-09-620-312D-1019
; Sequence 1019, Application US/09620312D
; Patent No. 6566652
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunru
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 656662el Nucleic Acids and
; FILE REFERENCE: 784CIP28
; POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: PC FL_genes Version 1.0
; SEQ ID NO 1019
; LENGTH: 1477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(753)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1477)
; OTHER INFORMATION: n = a,t,c or g
; US-09-620-312D-1019

Query Match 3.3%; Score 44.8; DB 4; Length 1477;
Best Local Similarity 52.0%; Pred. No. 0.0085;
Matches 128; Conservative 0; Mismatches 112; Indels 6; Gaps 1;

Qy 295 CCAAGCGGTGATGATGTCACATCCCTCGGTCGGGATCCAGATCCGACAA 354
Db 442 CCAATGGGCTCTATGTGGGTTCCCTGACCTCAATATCACTGAAGCATGCTCCGGGC 501
Qy 355 ATGTTGGCCAAATTTGTAATAATATTAATGATGTTGAATTAAT---TTTAATGAGCG 408
Db 502 ATCTTGAGCCCTTTGTAATAATTAATATATGCTGATGAAGACTCAGATTAAGGC 561
Qy 409 GGCTGAGGAGATTTGTTGTAATCTTGAATATGTCGATGCGAGACAGGCGAGG 468
Db 562 CGCTTAAGATTAATGTTTATCATCATGCTCTGATTTCTAGTGTGCGCGGCGGCTTG 621
Qy 469 GAGAAATTCAGCGTACCGGTGATGAGAGGCGGTAATAATTCAGGTTAATAATGAGAGCA 528
Db 622 GAACAGTTGAATGGGTTTGAAGCTTGCTGTGACCTTAAGAGGTTGGCCATGATGAG 681

Oy 529 CGCTG 534
||
Db 682 CGACTG 687

Search completed: January 15, 2004, 07:35:08
Job time : 113 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 15, 2004, 07:35:14 / Search time 631 Seconds
(without alignments)
65.784 Million cell updates/sec

Title: US-09-809-545a-2
Perfect score: 1086
Sequence: 1 MTRKKAVPNTGKMLNPVY.....VLSSLOASTYOGGYNRFAPY 203

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 762491 seqs, 20448190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppa/PCF_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubppa/PCFUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1086	100.0	203	10 US-09-809-545a-2	Sequence 2, Appl1
2	551	50.7	330	9 US-09-794-591-2	Sequence 2, Appl1
3	519	47.8	450	12 US-10-094-749-1926	Sequence 1926, Ap
4	288	26.5	366	12 US-10-359-385-2	Sequence 2, Appl1
5	116	10.7	3063	12 US-10-301-822-26	Sequence 26, Appl1
6	116	10.7	3063	15 US-10-177-293-61	Sequence 61, Appl1
7	116	10.7	3063	15 US-10-177-293-63	Sequence 63, Appl1
8	96	8.8	388	12 US-10-012-952A-172	Sequence 172, App
9	96	8.8	760	8 US-08-754-111B-2	Sequence 2, Appl1
10	94.5	8.7	950	12 US-10-108-260A-4492	Sequence 4492, Ap
11	93	8.6	692	15 US-10-156-761-14649	Sequence 14649, A
12	92.5	8.5	919	15 US-10-128-714-8387	Sequence 8387, Ap
13	92	8.5	351	12 US-10-029-386-32088	Sequence 32088, A
14	90.5	8.3	481	15 US-10-156-761-12012	Sequence 12012, A
15	90	8.3	443	12 US-10-369-493-10023	Sequence 10023, A

16	89.5	8.2	342	15 US-10-156-761-11221	Sequence 11221, A
17	89	8.2	470	12 US-10-104-047-2022	Sequence 2022, Ap
18	88.5	8.1	363	15 US-10-156-761-10205	Sequence 10205, A
19	88	8.1	380	15 US-10-156-761-11952	Sequence 11952, A
20	88	8.1	216	12 US-10-224-999A-3475	Sequence 3475, Ap
21	87.5	8.1	620	15 US-10-156-761-7979	Sequence 7979, Ap
22	87	8.0	465	15 US-10-205-823-136	Sequence 136, App
23	87	8.0	235	12 US-10-329-079-43	Sequence 43, App
24	86.5	8.0	262	10 US-09-263-689-14	Sequence 14, Appl1
25	86.5	8.0	262	15 US-10-235-674-14	Sequence 14, Appl1
26	86.5	8.0	742	15 US-10-156-761-12153	Sequence 12153, A
27	86.5	8.0	4292	12 US-10-080-334-273	Sequence 273, App
28	86.5	8.0	4299	12 US-10-080-334-90	Sequence 271, App
29	86.5	8.0	4302	12 US-10-080-334-271	Sequence 272, App
30	86.5	8.0	4302	12 US-10-080-334-272	Sequence 20, Appl1
31	86	7.9	245	9 US-09-796-858-20	Sequence 20, Appl1
32	86	7.9	275	12 US-10-313-853-3	Sequence 3, Appl1
33	86	7.9	279	11 US-09-813-408-21	Sequence 21, Appl1
34	86	7.9	337	15 US-10-156-761-12003	Sequence 12003, A
35	86	7.9	518	12 US-10-369-493-3240	Sequence 3240, Ap
36	86	7.9	550	15 US-10-156-761-11905	Sequence 11905, A
37	86	7.9	853	12 US-10-369-493-15517	Sequence 15517, A
38	86	7.9	856	12 US-10-369-493-15889	Sequence 15889, A
39	86	7.9	856	12 US-10-369-493-16260	Sequence 16260, A
40	85	7.8	275	8 US-08-322-678-7	Sequence 7, Appl1
41	85	7.8	275	9 US-09-060-854B-3	Sequence 3, Appl1
42	85	7.8	275	10 US-09-976-414-7	Sequence 7, Appl1
43	85	7.8	275	12 US-10-324-152-1	Sequence 1, Appl1
44	85	7.8	275	12 US-09-824-607-1	Sequence 4, Appl1
45	85	7.8	275	12 US-10-242-549-4	

ALIGNMENTS

RESULT 1
US-09-809-545a-2
/ Sequence 2, Application US/09809545A
/ Patent No. US20020110804A1
/ GENERAL INFORMATION:
/ APPLICANT: Scanlon, Lawrence W.
/ APPLICANT: White, R. Tyler
/ TITLE OF INVENTION: SECRETED FACTORS
/ FILE REFERENCE: SCIOS.017A
/ CURRENT APPLICATION NUMBER: US/09/809,545A
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 203
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-09-809-545a-2

Query Match	100.0%	Score 1086	DB 10	Length 203
Best Local Similarity	100.0%	Pred. No. 1.4e-98		
Matches 203	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MTRKKAVPNTGKMLNPVGAIVSPDFYAGTVLLCOANQEGSSMSGSPSLVYTSAMFG	60	
DB	1	MTRKKAVPNTGKMLNPVGAIVSPDFYAGTVLLCOANQEGSSMSGSPSLVYTSAMFG	60	
QY	61	PEYPAATAAARGAHGRGRTVNTTPRAAPPPPIPAVGGVVOEPPYGGKLLQGGVA	120	
DB	61	PEYPAATAAARGAHGRGRTVNTTPRAAPPPPIPAVGGVVOEPPYGGKLLQGGVA	120	
QY	121	AVRYAOPFPATAAASDSYGRVYAADPYHTLAPAPYGVGAMNAPAPLTDKTSHAD	180	
DB	121	AVRYAOPFPATAAASDSYGRVYAADPYHTLAPAPYGVGAMNAPAPLTDKTSHAD	180	
QY	181	VELVLSLOASTYOGGYNRFAPY 203		
DB	181	VELVLSLOASTYOGGYNRFAPY 203		

	Query Match	Score	DB	Length
Best Local Similarity	50.7%;	551;	9;	330;
Matches	97.1%;	Pred. No. 7,7e+46;		
	Conservative	1;	Mismatches	2;
			Indels	0;
			Gaps	0;

	QY	DB	
1	MTNKKAVNPYNGKWLNVGVAVSPDDPYAGTIVLLCONNOEBSNYSQSSSLVYTSNAPG	60	
196	MTNKKTVPYNGKWLNVGVAVSPERYAGTIVLLCONNOEBSNYSAPSSLYVTSNAPG	255	
QY	61	FPYPATATAAAYRGALHGRGRTVYNTFRAAAAPPPIPAYGVTV	105
DB	256	FPYPATATAAAYRGALHGRGRTVYNTFRAAAAPPPIPAYGVTV	300

RESULT 5
US-10-301-822-26
; Sequence 26, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamackar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER
FILE REFERENCE: MM01-029P2RM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ. ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 26
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-301-822-26

Query Match 10.7%; Score 116; DB 12; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.058;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;
QY 50 SSLVYTSAMPGFPPYATATAAAYR---GAHLRGGRTV-----YNTFRRAA 92
DB 2078 NNVILOPQDTPY-KITVIAYVEDDGGHLTGNGRTVGLPPQNIHISDEWTRFRVSM 2136
QY 93 PPPPIYAGGVVYQEPYVGNKLLQ---GGYAAARYAOPPTATAAAYSDSYGRVYADPYH 149
DB 2137 DPEPSPVLGKYIKVYKPGVSNPEMEAFVGEWTSYTL----- 2171
QY 150 HTLAAPPTYGVGAMNAFA-----PLTDKTRSHADVDGLVLSLQASITYGGYNRF 200
DB 2172 HNINPSTTYDV---NVYAQYDSGLSVPLTDQGT-----LYLVNTDLKTYQIGMDTF 2220

RESULT 6
US-10-177-293-61
Sequence 61, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatte, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamackar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ. ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 61
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-61

Query Match 10.7%; Score 116; DB 15; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.058;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;
QY 50 SSLVYTSAMPGFPPYATATAAAYR---GAHLRGGRTV-----YNTFRRAA 92
DB 2078 NNVILOPQDTPY-KITVIAYVEDDGGHLTGNGRTVGLPPQNIHISDEWTRFRVSM 2136
QY 93 PPPPIYAGGVVYQEPYVGNKLLQ---GGYAAARYAOPPTATAAAYSDSYGRVYADPYH 149
DB 2137 DPEPSPVLGKYIKVYKPGVSNPEMEAFVGEWTSYTL----- 2171
QY 150 HTLAAPPTYGVGAMNAFA-----PLTDKTRSHADVDGLVLSLQASITYGGYNRF 200
DB 2172 HNINPSTTYDV---NVYAQYDSGLSVPLTDQGT-----LYLVNTDLKTYQIGMDTF 2220

RESULT 7
US-10-177-293-63
Sequence 63, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatte, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamackar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-63

Query Match 10.7%; Score 116; DB 15; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.058;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;

QY 50 SSLVTSAMPGEPPYPAATAAAAYR---GAHLRGGRVY-----YTFPAAA 92
DB 2078 NNVLQPLQPDTPY-KITVIAVYEDGDGCHLTGNGRTVGLLPQNIHISDEWYTRFRVSW 2136
QY 93 PPPPIPAYGVVYQEPYGNKLLQ---GVYAAVRYAPTRATAAAYSDYGRVYAADPYH 149
DB 2137 DPSPSPVLGKYIKYKPGVSGNEPMEAFVGEWTSYTL----- 2171
QY 150 HTLAPARTYGVGAMNAPF-----PLTDKTRSHADVDGLVLSLQASLYQGYNRF 200
DB 2172 HNLNPSITTYDV---NVYAAQYDSGLSVLTLTGCT-----LYNVTDKTKYQIGWTF 2220

RESULT 8

US-10-012-952A-172
Sequence 172; Application US/10012952A
Publication No. US20030175707A1
GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sel-Yu
TITLE OF INVENTION: Composition and Methods Relating to Prostate Specific Genes and F
FILE REFERENCE: DEX-0263
CURRENT APPLICATION NUMBER: US/10/012,952A
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/246,039
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.1
SEQ ID NO 172
LENGTH: 388
TYPE: PRT
ORGANISM: Homo sapiens
US-10-012-952A-172

Query Match 8.8%; Score 96; DB 12; Length 388;
Best Local Similarity 24.9%; Pred. No. 0.4;
Matches 59; Conservative 16; Mismatches 86; Indels 76; Gaps 11;

QY 21 GAVVSPDYAGTVLLQANDGSSMYSGPSSL-----VYTSAMPGEPPYPAATAAAAYRG 74
DB 67 GGNSTVAAAAAANAQ-CRNLMAHFAFLAGASAYSSA-PGEAFPSAAAAA 124
QY 75 AHLRGGRVYNTFRFAAAPPPIPAYGVVYQ-----EPVYGNKLLQGYAAYRY- 124
DB 125 A-----AAAAAASSSGRPGAGAGAAKQCSPCSAAAOSSGPAALPYGYFGSGYYP 180
QY 125 -----AQTPTATAA-----YSDS-----YGRVYAADPY 148
DB 181 CARMGPHNAIKSCAQFASAAAAAFADKYMDTAGPAAEFFSSPAKEFAFYHOGYAAAGPY 240
QY 149 HHTLAPARTY-----GVGAMNAPARTLDAKTRSHADVDGLVLSLQASLYQGYN 198
DB 241 HHN-OPMGYLDMPVYFGLGSPG-----ESRHEPLGPMESTYOPALPENGWN 286

RESULT 9

US-08-754-311B-2
Sequence 2; Application US/08754311B
Publication No. US20020004221A1
GENERAL INFORMATION:
APPLICANT: Bonini, Nancy M.
APPLICANT: Leiserson, William M.
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehm, Hobach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/754,311B
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/195,152
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-754-311B-2

Query Match 8.8%; Score 96; DB 8; Length 760;
Best Local Similarity 23.7%; Pred. No. 0.92; Mismatches 61; Indels 50; Gaps 6;
Matches 42; Conservative 24;

QY 42 GSSNY-----SGPSSLVYTSAMPGEPPYPAATAAAAYRGALHGRGRTVYNTFFAAA 92
DB 223 GSNLYGSSASNPLDGAIVAVNSAV-----AAAAAAYDGH-----DYYYNSMQOYT 272
QY 93 PPPPIPAYGVVYQEPYGNKLLQGYAAYRYAQTPTATAA----- 134
DB 273 PPPFYSYGTPYAAATTAARAKMEPGAAAAAAYLTPSYAASGNNNSQLYSSPYAGYNF 332
QY 135 -----YDSYGRVYAADPYHHTLAPAP-----TYGVG-AMNAPARTLDAKTRSHA 178
DB 333 GOODYGGYVNEQYNTSPANYSPYAVSSSSASHGHVVAASSLSLSPFDTHS 389

RESULT 10

US-10-108-260A-4492
Sequence 4492; Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: Helix Research Institute
TITLE OF INVENTION: No. US20040005560a1el full length cDNA
FILE REFERENCE: H1-40106
CURRENT APPLICATION NUMBER: US/10/108,260A
NUMBER OF SEQ ID NOS: 5458

SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4492
 LENGTH: 950
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-108-260A-4492

Query Match 8.7%; Score 94.5; DB 12; Length 950;
 Best Local Similarity 25.0%; Pred. No. 1.7;
 Matches 35; Conservative 15; Mismatches 51; Indels 39; Gaps 6;

QY 39 NQSSMSYSGPSSLLVYTSAMPGPYPATATAAAYGCAHLRGRTYNTFRRAAPPPPP 98
 DB 836 DQSEPPFPVPPGMYMTVLDPDGSFVP-----GGMALY-----APPPPLP 874
 QY 99 -----AYGVVYQEPYVYKLLQGGAAYRYAOPPTATAAASDSYGRVYADPYHHTL 152
 DB 875 NNSRPLTPTGVVYVPPGAPAPMYG-----PPPNPSITPTPWGVLHCNVPEHNL 925
 QY 153 APATYGVGAMNAFAP-LTD 171
 DB 926 VSGKTY--NSLSTLTPWTD 943

RESULT 11
 US-10-156-761-14649
 Sequence 14649, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHITOKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 PRIOR FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ. ID NOS: 15109
 SEQ. ID NO 14649
 LENGTH: 692
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-14649

Query Match 8.6%; Score 93; DB 15; Length 692;
 Best Local Similarity 31.1%; Pred. No. 1.6;
 Matches 42; Conservative 8; Mismatches 47; Indels 38; Gaps 8;

QY 42 GSSMSYSGPSSLLVYTSAMPGPYPATATAAAYG-----AHLRGRTYNTFRRAAP-- 93
 DB 329 GIGANGVPGGTGSGAGSAPSPPGATAGTGTGTPSEPPVGRPAAGSGGDPNAPYA 388
 QY 94 -PPPIYAGVVYQEPYVYKLLQGGAAYRYAOPPTA--TAAAY-----SDSYGRVYA 144
 DB 389 HDPATSYG-----QEP-----GAPRGPPTASPYGRSPTASYSQSPA 428
 QY 145 ADPYHHTLAPATYTG 159
 DB 429 ATPYADPTASP-YG 442

RESULT 12
 US-10-128-714-8387
 Sequence 8387, Application US/10128714
 Publication No. US20030119013A1
 GENERAL INFORMATION:

APPLICANT: Jiang, Bo
 APPLICANT: Hu, Wengqi
 APPLICANT: Tishkoff, Daniel
 APPLICANT: Zamudio, Carlos
 APPLICANT: Eroethkin, Alexey M
 APPLICANT: Lemieux, Sebastien M
 TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
 FILE REFERENCE: 10182-018-999
 CURRENT APPLICATION NUMBER: US/10/128,714
 CURRENT FILING DATE: 2002-04-23
 PRIOR APPLICATION NUMBER: US 60/285,697
 PRIOR FILING DATE: 2001-04-23
 PRIOR APPLICATION NUMBER: US 60/287,066
 PRIOR FILING DATE: 2001-04-27
 PRIOR APPLICATION NUMBER: US 60/295,890
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/303,899
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US 60/316,362
 PRIOR FILING DATE: 2001-08-31
 NUMBER OF SEQ. ID NOS: 8603
 SOFTWARE: PatentIn version 3.1
 SEQ. ID NO 8387
 LENGTH: 919
 TYPE: PRT
 ORGANISM: Aspergillus fumigatus
 US-10-128-714-8387

Query Match 8.5%; Score 92.5; DB 15; Length 919;
 Best Local Similarity 28.6%; Pred. No. 2.6;
 Matches 36; Conservative 10; Mismatches 61; Indels 19; Gaps 5;

QY 57 AMPGPYPATATAAAYRGHLEGRRTYNTFRRAAPPPPIYAGVVYQEPYVYKLLQ 116
 DB 47 AYAGEAFBIGSANAALGGQLPAGS--YGAY-----PPQQAAG--YQGVYGADEPQ 96
 QY 117 GGAAYRYAOPPTATAAASDSYGRVYADPYHHTLAPATYGVGAMNAFAPL----- 169
 DB 97 NMAAABGYATPTPTGIAQNTQGFAMGVTD--HLMPQPQAAYAPQAPRPVPLNQLYP 154
 QY 170 TDAKTR 175
 DB 155 TDLTQ 160

RESULT 13
 US-10-029-386-32088
 Sequence 32088, Application US/10029386
 Publication No. US20030194704A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David K.
 APPLICANT: Hanzel, David K.
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: A60MICA-X-2
 CURRENT APPLICATION NUMBER: US/10/029,386
 CURRENT FILING DATE: 2001-12-20
 NUMBER OF SEQ. ID NOS: 34288
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 SEQ. ID NO 32088
 LENGTH: 351
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO L39891.1
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.4
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9

OTHER INFORMATION: SWISSPROT HIT: P98161, EVALUATE 5.00e-39
US-10-029-386-32088

Query Match
Best Local Similarity 8.5%; Score 92; DB 12; Length 351;
Matches 58; Conservative 24; Mismatches 83; Indels 72; Gaps 11;

QY 18 PVVGAAY--SPPEYAGTVLLCOANQEGSSMYSGPSSLVYTSAMPFPYPA-----66
DB 125 PLIGEEYVACLFDNNSGTV-----AAVSSAAHEGLLOEACAFCFST 168
QY 67 ---TAAAYRGALHGRGRTVYNTFR-----AAAPPPPIAYGQVYQEPVY-----110
DB 169 GQGLAALSEQGWCICGAAGPSSASFACTSLCSGPPPPAPTCRGPTLLQHVFPASPQATL 228
QY 111 ---GNKLLQGGYAAVRYAOTPATTA--YSDSYGRYAADP-----YHHTLAP 154
DB 229 VGPBGLPGLASQGLAFHIAAPLPYATRTWDPDGSAAVEDAAGPASHRYVLPGRYHTVAVL 288
QY 155 APTVGVGAMNAPAPLPTDAKTRSHADVDVGLV-----SSIQASITY-QGGVNRFPAPY 203
DB 289 A----LGAGSALLG-IDVQVEAPAPALELVCPSSVGSDESLSIQNRGSSGLEAY 340

RESULT 14
US-10-156-761-12012

Sequence 12012, Application US/10156761
Publication No. US20030119018A1

GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12012
LENGTH: 481
TYPE: PRT
ORGANISM: Streptomyces avermectilis
US-10-156-761-12012

Query Match
Best Local Similarity 8.3%; Score 90.5; DB 15; Length 481;
Matches 47; Conservative 11; Mismatches 75; Indels 35; Gaps 7;

QY 26 PDPVAGTVLLCOANQEGSSMYSGPSS---LVYTS-AMPGPYPATATAAAYRGALHGR 80
DB 298 PDESSGAVLIRFGAGDAGGASGESGRKTCISQSSBGVGTAEFGDAMGASVAAADDDG 357
QY 81 GRVYNTFRFAAAPPPPIPAYG-----GVVYQEPVYGNKLLQGGYAAVRYAOTPAT 131
DB 358 G-----APELVVGAPGEGVGSLSKAGSVTVLDGTGEGPLSGVT---YTONTPCI 404
QY 132 --AAVSDSYGRVYAADPYHHTLAPAPTYGVGAMNA-----FAPLTD 171
DB 405 PGTAETADRFAGATLTAGVHGRBPDILAIGAPGENAAKGWVYVPTTD 452

RESULT 15
US-10-369-493-10023
Sequence 10023, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10023
LENGTH: 443
TYPE: PRT
ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-10023

Query Match
Best Local Similarity 8.3%; Score 90; DB 12; Length 443;
Matches 49; Conservative 14; Mismatches 56; Indels 68; Gaps 11;

QY 17 NPVGAAYSPDPFYAGT-----VLLCOANQEGSSMYSGPSSLVYTSAMPFPYPAATA 69
DB 48 SPVAGVY--TEIYAGVADADVGVAGVLCVDAQGSARAVAPAK---PAAEPA-PAPAVATA 101
QY 70 AAYRGALHGRGRTVYNTFRFAAAPPPPIPA--YGVVYQEPV-----109
DB 102 ATPAPA-----VATPAPTVVAPPSGGAALSPAVRKLAEHGLDATTQIPAT 147
QY 110 -YGNKLLQGGYAAV-----RYAOTPATTAAYSDSYGRVYAADPYHHTLAPAPTYGVG 161
DB 148 GSGGRLTKGDVLAYLEQPKAPAPTAAPTAPTAAPT-----APT---TPADAPM-----194
QY 162 ANNAPAP 168
DB 195 ATPALAP 201

Search completed: January 15, 2004, 09:02:14
Job time : 634 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 15, 2004, 06:09:58 ; Search time 45 Seconds
(without alignments)
190.869 Million cell updates/sec

Title: US-09-809-545A-2

Perfect score: 1086
Sequence: 1 MTNKKAVNPYNTGKMLNPVY.....VLSSQASIVQSGYNFAPY 203

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	50.7	330	3 US-09-145-391-2	Sequence 2, Appl1
2	288	26.5	366	3 US-09-176-657-2	Sequence 2, Appl1
3	288	26.5	366	4 US-09-421-299-2	Sequence 2, Appl1
4	96	8.8	760	1 US-08-195-152-2	Sequence 2, Appl1
5	94	8.7	349	4 US-09-143-011B-1	Sequence 1, Appl1
6	93	8.6	444	3 US-09-252-292C-27	Sequence 2, Appl1
7	92.5	8.5	362	1 US-08-437-027-21	Sequence 2, Appl1
8	92.5	8.5	365	1 US-08-437-027-20	Sequence 2, Appl1
9	92.5	8.5	656	2 US-08-343-443B-2	Sequence 2, Appl1
10	92.5	8.5	656	2 US-09-214-564A-4	Sequence 2, Appl1
11	91	8.4	346	4 US-09-343-011B-2	Sequence 2, Appl1
12	88.5	8.1	902	4 US-09-252-991A-19897	Sequence 19897, A
13	87.5	8.1	980	4 US-09-442-100-8	Sequence 8, Appl1
14	87.5	8.1	980	4 US-08-939-106-8	Sequence 8, Appl1
15	87	8.0	379	1 US-08-552-142A-11	Sequence 11, Appl1
16	86.5	8.0	262	3 US-08-946-914-14	Sequence 14, Appl1
17	86.5	8.0	262	4 US-09-666-450-14	Sequence 14, Appl1
18	86.5	8.0	4302	3 US-08-658-136-5	Sequence 5, Appl1
19	86.5	8.0	4302	4 US-09-052-469-8	Sequence 8, Appl1
20	86.5	8.0	4302	4 US-08-422-582-8	Sequence 8, Appl1
21	86.5	8.0	4339	4 US-09-052-469-6	Sequence 6, Appl1
22	86.5	8.0	4339	4 US-08-422-582-6	Sequence 6, Appl1
23	86	7.9	207	4 US-09-336-536-50	Sequence 50, Appl1
24	86	7.9	245	4 US-09-336-536-48	Sequence 48, Appl1
25	85	7.8	273	4 US-09-088-912-1	Sequence 1, Appl1
26	85	7.8	275	1 US-08-431-387-3	Sequence 3, Appl1
27	85	7.8	275	1 US-08-322-677A-7	Sequence 7, Appl1

28	85	7.8	275	1 US-08-322-676-7	Sequence 7, Appl1
29	85	7.8	275	1 US-08-460-343B-74	Sequence 74, Appl1
30	85	7.8	275	1 US-08-398-028B-74	Sequence 74, Appl1
31	85	7.8	275	2 US-08-504-265B-90	Sequence 90, Appl1
32	85	7.8	275	2 US-08-140-083A-9	Sequence 9, Appl1
33	85	7.8	275	2 US-08-865-203-8	Sequence 8, Appl1
34	85	7.8	275	2 US-09-135-658-3	Sequence 3, Appl1
35	85	7.8	275	2 US-07-849-420-8	Sequence 8, Appl1
36	85	7.8	275	3 US-08-898-218-7	Sequence 7, Appl1
37	85	7.8	275	3 US-08-848-793-7	Sequence 7, Appl1
38	85	7.8	275	3 US-09-253-854-8	Sequence 8, Appl1
39	85	7.8	275	3 US-08-955-424-8	Sequence 8, Appl1
40	85	7.8	275	4 US-09-178-153-3	Sequence 3, Appl1
41	85	7.8	275	4 US-09-445-270-2	Sequence 2, Appl1
42	85	7.8	275	4 US-09-467-536A-2	Sequence 2, Appl1
43	85	7.8	275	4 US-09-234-957-2	Sequence 2, Appl1
44	85	7.8	275	4 US-08-394-011-1	Sequence 1, Appl1
45	85	7.8	275	4 US-08-397-329-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
; US-09-145-391-2
; Sequence 2, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Pulist, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/145,391
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-145-391-2

Query Match      50.7% Score 551; DB 3; Length 330;
Best Local Similarity 97.1%; Pred. No. 3 4e-48;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 MTNKKAVNPYNTGKMLNPVGAIVSDDPYAGTVLLCOANQEGSSMYSGPSSLVTSAMG 60
      |||||
DB      196 MTNKKAVNPYNTGKMLNPVGAIVSDDPYAGTVLLCOANQEGSSMYSGPSSLVTSAMG 255
      |||||

QY      61 FYPPATTAAYRGALRGRTVYNTFPAAPPPPIPAVGIVY 105
      |||||
DB      256 FYPPATTAAYRGALRGRTVYNTFPAAPPPPIPAVGIVY 300
      |||||

RESULT 2
; US-09-176-657-2
; Sequence 2, Application US/09176657
; Patent No. 6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176,657
; CURRENT FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
```

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; SEQ ID NO 2
; LENGTH: 366
; TYPE: prt
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-176-657-2

```

Query Match	26.5%	Score 288;	DB 3;	Length 366;
Best Local Similarity	48.9%	Pred. No. 2,4e-21;		
Matches 68;	Conservative 11;	Mismatches 54;	Indels 6;	Gaps 4

Qy MTKKKAVNPATINCMKINPVGAVGYSDFPAAGVILLCOAN--QEGSMVSGSSSL--VYTS 56
Db MTKKKAVTPAANGMKLSPVGVAVGPELVAAS PQADVSLGNDAAVPLSGGGINTYIPL 190

Qy AMGGEPPP-AAITAAAYRGAGHLRGKRTTYNTFFAAAPPPPIPAVGIVGEPYGGKLL 115
Db IIGGPPPTATTAAPAFRGAGHLRGKRTTYGAVR-AVPPITAPALPGVDGPTDMHSLL 306

QY 116 QGGYAYRYAQTPTATAA 134
| : | | |
DB 309 QPQPELLQPLQLTVTMA 327

RESULT 3
US-09-421-299-2

```

sequence 4, Application US/05421295
Patent No. 6524579
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Aina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/421,299
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: 09/176,657
EARLIER FILING DATE: 1998-10-21
NUMBER OF SEQ. ID NOS.: 9
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 366
TYPE: PRF
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 1250374
US-09-421-299-2

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Query Match	26.5%	Score 288	DB 4	Length 366
Best Local Similarity	48.9%	Pred. No. 2.4e-21		
Matches 68; Conservative	11; Mismatches	54;	Indels 6;	Gaps 4

Oy 1 MTKKCAVNPATNGCKINPNVGVAYSPDPFAGTTLCOAA--QEGSSMTSGSSSL--VYTS 56
| | | | | : | | | | | : | | | | | : | | | | | :
Db MTNKKWVTLPFANGKRLSPVVGAVYGPELYAASFOADVSLGNDAAVPISGRGINVTYPL 249

Oy 57 AMDEPPRP-AATAAAAYRGAIHGRGRTYNTFRPAAAPRPIPAYGVVOEPVYGNLTL 118
| | | | | : | | | | | : | | | | | : | | | | | :
Db TTFEPRPTATTAARFGIHLNRGGRITVGAVR-AYPTALPAIFPGMDQPTDMSILL 308

Oy 116 QGGYAAYRYAOPTPATAA 134
| | | | | : | | | | | : | | | | | :
Db QPQPPLLQPLQPLTVYMA 327

RESULT 4
US-08-195-152-2
; Sequence 2, Application US/08195152
; Patent No. 5679541

GENERAL INFORMATION:
APPLICANT: Bonini, Nancy M.
APPLICANT: Leiserson, William M.
APPLICANT: Benzer, Seymour
TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESS: Flehr, Hobbach, Test, Abritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California

```

;      COUNTRY:  United States
;
;      ZIP:  94111-4187
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;

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;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.2
;
; CURRENT APPLICATION DATA:
;
; 08/06/1985 173

```

APPLICATION NUMBER: US/08/195,152
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Thomas J. Dischard P

NAME: IIECADIU, RICHARD F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 791-1080

TELEPHONE: (415) 398-3249
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-195-152-2

INSTRUMENTED DATE: 1995-08-08

Query Match 8.8%; Score 96; DB 1; Length 760

Best Local Similarity 23.7%; Pred. No. 0.23;

Matches	42;	Conservative	24;	Mismatches	61;	Indels	50;	Gaps	6
Qy	42	GSSMY-----	SGPSLVTYSAMPEFP	PATATAAAYGAH	RGRGRVTYNTFR	AAA	92		
		:	:	:			:	:	

Db 223 GSNLYCCSSASNPIDGGAAVNSAV-----AAAAAVYDGKH-----DYRYYSMSQQT 272

Qy 93 PPPPIPAYGAVYQEPVYGNKLGGVAAYRAOPTATAA----- 134

```
Dd      273. PPFYSGYGCTPAAALAAQAQMGEGAAAAAAYLTPTSYAAGNNNSQLVSSPYAGINNF
Qy      135 -----YSDSGRVYAADPYHHTLAPD-----TYGVG-AMNAFAPLTDAKTRSHA 178
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Db 333 GQDDYGGYINQYGNYYSPANSPYAVSSPSSASHCHGPHVAASNNLSIESPTDTHS 389

```

US-09-343-011B-1
; Sequence 1. Application US/05343011B
; Patent No. 6300473
; GENERAL INFORMATION:
; APPLICANT: Stephane Richard
; TITLE OF INVENTION: SLM-1 AND SLM-2; NOVEL
; TITLE OF INVENTION: SAM68-LIKE MAMMALIAN PROTEINS
; FILE REFERENCE: A32561
; CURRENT APPLICATION NUMBER: US/09/343.011B
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: CA 2265271
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 349

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Page 2

TYPE: PRT
ORGANISM: Mus musculus
US-09-343-011B-1

Query Match
Best Local Similarity 30.7%; Score 94; DB 4; Length 349;
Matches 54; Conservative 11; Mismatches 51; Indels 60; Gaps 12;

QY 73 RGAHLRGRTVNTF-----RAAAPPPIPAGGVVQEPVGNKLOG----- 117
DB 186 RGRGIRGRIRITPTASRGRGAVPPPPRGVLTFR---GTYTRGALPPPIARGV 242
QY 118 -----GYAA--YRVAQPTPATTA--AYSDSYGRVYAADPY--HTTLAPAPT----- 157
DB 243 PTPRARGTAAPVGR-APPPADAYAEYGDGGEYDDQTYEAVDMSVYPTQSVPE 301
QY 158 ---YVGC---ANNAFPLTDATKTRSHADVGLVLSLOA---SITYGGINRPAFY 203
DB 302 YVDYGHGVNBDAYDVAPEEMATTR-----SLKAPPPRSARGY-REHPY 346

RESULT 6

US-09-252-292C-27
Sequence 27, Application US/0925292C
Patent No. 6245968
GENERAL INFORMATION:
APPLICANT: Boudec, Philippe
APPLICANT: Rodgers, Matthew
TITLE OF INVENTION: Mutated hydroxyphenylpyruvate dioxygenase, DNA
TITLE OF INVENTION: sequence and isolation of plants which contain such a
FILE REFERENCE: 5500*11
CURRENT APPLICATION NUMBER: US/09/252,292C
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 08/982,772
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 27
LENGTH: 444
TYPE: PRT
ORGANISM: Zea mays
US-09-252-292C-27

Query Match
Best Local Similarity 22.8%; Score 93; DB 3; Length 444;
Matches 51; Conservative 22; Mismatches 69; Indels 82; Gaps 10;

QY 55 TSAMPGRPYPAATAAAYRGALRG--RGRVTYNTFRAPPPPIPAYGV-----V 104
DB 112 TAAIPSSAAARFPAADHGLAVAVALRVADADEDARASVAAAGARAFGPVLDGRGRL 171
QY 105 YQBPVGNKLLQGGYAAVRYAOPTPATTAAYSDSYGV-----YAADPYHH-----T 151
DB 172 AEVEIVGDVLR--YVSY-----PDGAAGEPFLPGFEBVAPGAADYGLSFDHIVGNVPE 225
QY 152 LAPAPY-----GVGAM-----NAPALTD---AKTRSH 177
DB 226 LAPAAVYAFAGFTGFHEFAEFTTEDVGTAEGLNSMVLANNSEVLLPLNPNVHGTGRSQ 285
QY 178 -----ADYGLVLSLOASTIYOGGINRPAF 202
DB 286 IQFLDHHGGPGVQHMALASGDVLRITLREMQARSAMGCFEFMAP 329

RESULT 7

US-08-437-027-21
Sequence 21, Application US/08437027
Patent No. 5670317
GENERAL INFORMATION:
APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William

TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
TITLE OF INVENTION: SMALL ROUND CELL TUMOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,027
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 46416/JPW/CCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-437-027-21

Query Match
Best Local Similarity 27.9%; Score 92.5; DB 1; Length 362;
Matches 48; Conservative 10; Mismatches 73; Indels 41; Gaps 9;

QY 29 YAGTVLLQA-NOBSSMYSGSSLVYTSNMGFPYPATATAAARGALRGRTVNT 87
DB 29 YAGTT---QAYGQSGYGTGPTDVSYTOQTATYGGTAVTSY-----GQPTGYTT 79
QY 88 PRAAPPPPIPAYGVVQEPVGNKLLQGGYAAVRYAOPTPATTAAYSDSYGRVYADP 147
DB 80 -----PTAPQ---AYSQPVGY-----GTGADTTTATYTTQA-----SYAQS 116
QY 148 YHHTLAPAPTYGVGAMNAPAPLTDKTRSHADVGLVLSLOASTIYOGGINR 199
DB 117 AVGTQPAYVAYQ-----QPAATAPTRPDGNKPTETSPQSS--TGGYNQ 160

RESULT 8

US-08-437-027-20
Sequence 20, Application US/08437027
Patent No. 5670317
GENERAL INFORMATION:
APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William
TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
TITLE OF INVENTION: SMALL ROUND CELL TUMOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,027
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 46416/JPM/CCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-437-027-20

Query Match 8.5%; Score 92.5; DB 1; Length 365;
Best Local Similarity 27.9%; Pred. No. 0.19; Indels 41; Gaps 9;
Matches 48; Conservative 10; Mismatches 73;

QY 29 YAGTVLLCOA-NOEGSSMYSGPSLVYTSAMPFPYPAATAAAYRGALHGRGRVYNT 87
DB 29 YAGTT---QAYGQSGYGTGPTDVSTQAQTATYGTATVSY-----GQPTGYTT 79
QY 88 FRAAAPPPPIPAVGAVVYOEPPVGNKLLGGVAAVYAOPTPATTAAYSDSYGRVYAADP 147
DB 80 -----PTAPQ-----AYSQPVQGY-----GTGAYDTTATVTTTQA-----SYAQS 116

QY 148 YHHTLAAPTYGVGAMNAPFLTDKTRSHADVGLVLSLSQASIVGGYNR 199
DB 117 AYGTQPAYPAYGQ-----OPATAPTPRPDGKNKPTETSPQSS--TGGYNQ 160

RESULT 9
US-08-343-443B-2
Sequence 2, Application US/08343443B
Patent No. 5968734
GENERAL INFORMATION:
APPLICANT: Aurias, Alain
APPLICANT: Delattre, Olivier
APPLICANT: Desmaze, Chantal
APPLICANT: Melot, Thomas
APPLICANT: Peter, Martine
APPLICANT: Ploougaetel, Beatrice
APPLICANT: Thomas, Gilles
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
TITLE OF INVENTION: TRANSLATIONS
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
CITY: Philadelphia
STATE: PA
COUNTRY: PA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989,6121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 656 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-343-443B-2

Query Match 8.5%; Score 92.5; DB 2; Length 656;
Best Local Similarity 27.9%; Pred. No. 0.43; Indels 41; Gaps 9;
Matches 48; Conservative 10; Mismatches 73;

QY 29 YAGTVLLCOA-NOEGSSMYSGPSLVYTSAMPFPYPAATAAAYRGALHGRGRVYNT 87
DB 29 YAGTT---QAYGQSGYGTGPTDVSTQAQTATYGTATVSY-----GQPTGYTT 79
QY 88 FRAAAPPPPIPAVGAVVYOEPPVGNKLLGGVAAVYAOPTPATTAAYSDSYGRVYAADP 147
DB 80 -----PTAPQ-----AYSQPVQGY-----GTGAYDTTATVTTTQA-----SYAQS 116

QY 148 YHHTLAAPTYGVGAMNAPFLTDKTRSHADVGLVLSLSQASIVGGYNR 199
DB 117 AYGTQPAYPAYGQ-----OPATAPTPRPDGKNKPTETSPQSS--TGGYNQ 160

RESULT 10
US-09-214-564A-4
Sequence 4, Application US/09214564A
Patent No. 6150515
GENERAL INFORMATION:
APPLICANT: Sharp, Phillip A.
APPLICANT: Zhou, Qiang
TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
TITLE OF INVENTION: Elongation By HIV-1 TAT
FILE REFERENCE: M0656/7042
CURRENT APPLICATION NUMBER: US/09/214,564A
CURRENT FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: US 60/021,218
PRIOR FILING DATE: 1996-07-03
PRIOR APPLICATION NUMBER: US 60/033,152
PRIOR FILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: PCT/US97/11713
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 656
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-564A-4
Query Match 8.5%; Score 92.5; DB 3; Length 656;
Best Local Similarity 27.9%; Pred. No. 0.43; Indels 41; Gaps 9;
Matches 48; Conservative 10; Mismatches 73;

Db 80 -----PTAPQ-----AYSQPVQGY-----GTGAYDTTATVTTQA-----SYAQS 116
Qy 148 YHHTLAPATPYGVGAMNAPFLDTAKTRSHADVDGLVLSLQASIVQGYNR 199
Db 117 AYGTOPAYPAVQ-----OPATATPTRPDGNKPTETSOPOS--TGTYNQ 160

RESULT 11

US-09-343-011B-2
; Sequence 2, Application US/09343011B
; Patent No. 6306473
; GENERAL INFORMATION:
; APPLICANT: Stephane Richard
; TITLE OF INVENTION: SIM-1 AND SIM-2; NOVEL
; TITLE OF INVENTION: SAME8-LIKE MAMMALIAN PROTEINS
; FILE REFERENCE: A32561
; CURRENT APPLICATION NUMBER: US/09/343.011B
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: CA 2265271
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-343-011B-2

Query Match 8.4%; Score 91; DB 4; Length 346;
Best Local Similarity 33.3%; Pred. No. 0.26;
Matches 32; Conservative 8; Mismatches 46; Indels 10; Gaps 4;

Qy 60 GFPPATATAAAYRGALHRRG-----RTVYNT-FRAAAPPPPIRGVYQEPYGN 112
Db 221 GTPPRGVLT-RGPVSRKGLTTPRAKGVPPGYRPPPPPTQETGYDYDDG-YGT 277
Qy 113 KLLGGYAAAYRAOPTATAAAYSDSYGRVYADPY 148
Db 278 AYDEQSYDSDYSTYRQSNADYDYGHGLSEAY 313

RESULT 12

US-09-252-991A-19897
; Sequence 19897, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19897
; LENGTH: 902
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19897

Query Match 8.1%; Score 88.5; DB 4; Length 902;
Best Local Similarity 23.6%; Pred. No. 1.7;
Matches 54; Conservative 19; Mismatches 75; Indels 81; Gaps 11;

Qy 26 PDPTAGTVLLCOANQEGSSMYSGP-----SLVYTGMRGFPYPATATAAYR 73
Db 92 PGWYAGS-----RRNSGPRGPRRAGRATLPGSARMAARWAPGSPRPSSPACR 146
Qy 74 GA-----HLGR-----GRTVNTFPAA--APPPIP-----AY 100

Db 147 GTATGWPRAADRHSAGCGPERRIADEGKRAPDGRPPGPRGPAP1RHWGRGGRPASRAC 206
Qy 101 GGVVQEPYGNKKLQGGYAAARYAQPATATAAYSDSYGRVYADPYHHTLAP----- 154
Db 207 ASVPOQLGTRQDDVVOG-----EAEVLEQRGRRLBAGHADAPVETDVL 253
Qy 155 APTVGVAMNAPFLDTAKT---RSHADVDGLVLSLQASIVQGYNR 200
Db 254 VPVVGMGGLDG-----DARADPHRQHLGLVGLLVDA-----GAMHRY 293

RESULT 13

US-09-442-100-8
; Sequence 8, Application US/09442100
; Patent No. 6159193
; GENERAL INFORMATION:
; APPLICANT: Xu, Tian
; APPLICANT: Tao, Wufan
; APPLICANT: Wang, Weiyl
; APPLICANT: Zhang, Sheng
; APPLICANT: Yu, Wan
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/442.100
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/411,111
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18, 872
REFERENCE/DOCKET NUMBER: 6523-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 980 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-442-100-8

Query Match 8.1%; Score 87.5; DB 4; Length 980;
Best Local Similarity 25.4%; Pred. No. 2.4;
Matches 50; Conservative 21; Mismatches 81; Indels 45; Gaps 9;

Qy 26 PDPTAGTVLLCOANQEGSSMYSGPSSLVYTSMPP---GFYPATATAAYRGALHRRG 81
Db 108 PSFEGTGELPSYHOLGCAHYEGPAL---EEMPROYDLFLPPG--AGAGTHGAQAHQHP 162
Qy 82 RTVYNTFPRAAAPPPPIP-----AYGVVYQEPVYG-----NKLQGGYAAARYAQAQ--- 126
Db 163 PKGYST--AVPESAHPGTHYRGHLSQSGYGVORSSSPFNKTPPDATYSMAQAQGP 220
Qy 127 ---PTPATATAAYSDSYGRVYADPYHHTLAPATYG---VGAMNAPFLDTAKTRSHAD 179

Db 221 PASLTFPAHAGLYTASHHKKPAATPPGAHPLHVLCTGRPTFTGSSSAQAVLAPSR----- 274
QY 180 DVGVLSSLOASIQOG 196
Db 275 -----NSLNADLYELG 285

RESULT 14

US-08-939-106-8
Sequence 8, Application US/08939106
Patent No. 6559285
GENERAL INFORMATION:
APPLICANT: Yale University
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,106
FILING DATE: 26-May-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-007-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 980 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-939-106-8

Query Match 8.1%; Score 87.5; DB 4; Length 980;
Best Local Similarity 25.4%; Pred. No. 2.4; Mismatches 81; Indels 45; Gaps 9;
Matches 50; Conservative 21; Mismatches 81; Indels 45; Gaps 9;
QY 26 PDFAVAGVLLCOAQEGSSSMYSGPSSLYVTSAMP-----GPPYPAATAAAVGAHLRGRG 81
Db 108 PSFSGTGALPSYHQLGAGNVEGPAL---EMERQYDPLFG--ACAGTHGAQAHQHP 162
QY 82 RTVNTTFPAAAPPPPIP-----AYGCVTVQEPVYG-----NKLLQGGYAAVRYAQ--- 126
Db 163 PKGVST--AVEPSSAHFPGTHYGRGHLSEQSGYGVQSSSPONTKPPDAYSSMAKAQGGP 220
QY 127 -----PTPATAAAYSDSYGRVVAADPYHHTLAPAPTYG---VGAMNAFAPLTDATKRSHAD 179
Db 221 PASLTFPAHAGLYTASHHKKPAATPPGAHPLHVLCTGRPTFTGSSSAQAVLAPSR----- 274
QY 180 DVGVLSSLOASIQOG 196
Db 275 -----NSLNADLYELG 285

RESULT 15
US-08-552-142A-11

Sequence 11, Application US/08552142A
Patent No. 5695995
GENERAL INFORMATION:
APPLICANT: Weintraub, Harold M.
APPLICANT: Lee, Jacqueline B.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Hollenberg, Stanley M.
TITLE OF INVENTION: Neurogenic Differentiation (NeuroD) Genes
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/552,142A
FILING DATE: 02-NOV-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/05741
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: PHCR-1-8933
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-225-0709
TELEFAX: 206-682-8100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-552-142A-11

Query Match 8.0%; Score 87; DB 1; Length 379;
Best Local Similarity 20.8%; Pred. No. 0.74;
Matches 38; Conservative 23; Mismatches 73; Indels 48; Gaps 6;
QY 14 WKLNPPVGVANYSDFPFAVGYLLC-----QANQEGSSMYSGP 49
Db 171 WALSEILRSKRDPLVSYVOTLLCKLSQPTTNLVAGCLQNSNPLTEQGRDAXRPHGS 230
QY 50 SSLVYTSAMPGPFPAPPA-----TAAAYRGHLAGRGR--TVVNT--FPAAPPPPIPA 99
Db 231 GG---PFAAMPPIPPCSRGGRVTPGAAAWAAAGRLRTHGICAYETLVAAAGCGGASPD 287
QY 100 YGCVTVQEPYGNKLLQGGYAAVRYAQPPTATAAAYSDSYGRVVAADPYHHTLAPAPTYG 159
Db 288 YNSEYEGPLSPPLCLNNGNFSNLQDSEPDHEKSYHVS-----MHYSGCPGSRHG 336
QY 160 VG 161
Db 337 HG 338

Search completed: January 15, 2004, 08:41:50
Job time : 50 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2004, 08:51:30 ; Search time 263.148 Seconds
(without alignments)
2719.103 Million cell updates/sec

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Perfect score: 1086
Sequence: 1 MTNKKAVNPNYNGMKLNPV.....VLSSIQASTYGGCYNRFAPY 203

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2324096 segs, 1762381658 residues
Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cg2_1/USPTO.spool_p/US09809545/rnatc_15012004_061052_2510/app.query.faesta_1.718
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-FCGAPOP=6 -FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

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1	1086	100.0	1340	10	US-09-809-545A-1	Sequence 1, Appli
2	955	87.9	2372	9	US-09-794-591-1	Sequence 1, Appli
3	519	47.8	1558	13	US-10-094-749-287	Sequence 287, App
4	500.5	46.1	1843	11	US-09-919-039-266	Sequence 266, App
5	467.5	43.0	1506	13	US-10-359-385-5	Sequence 5, Appli
6	231.5	21.3	2397	12	US-10-104-047-559	Sequence 654, App
7	116	10.7	11447	13	US-10-301-822-55	Sequence 25, Appli
8	116	10.7	11447	15	US-10-177-293-60	Sequence 60, Appli
9	116	10.7	11560	15	US-10-177-293-62	Sequence 62, Appli
10	116	10.7	11657	15	US-10-198-846-11039	Sequence 11039, A
11	108.5	10.0	6830	14	US-10-098-841-226	Sequence 226, App
12	107	9.9	895	9	US-09-770-445-481	Sequence 481, App
13	103	9.5	7053	13	US-10-252-157-219	Sequence 219, App
14	102.5	9.4	1089	15	US-10-156-761-16555	Sequence 2655, App
15	102.5	9.4	9025608	15	US-10-156-761-1	Sequence 1, Appli
16	99.5	9.2	5643	13	US-10-012-952A-43	Sequence 43, Appli
17	99	9.1	60	13	US-09-908-975-7420	Sequence 7420, Ap
18	99	9.1	464	13	US-10-027-632-18118	Sequence 18118, A
19	99	9.1	464	14	US-10-027-632-18118	Sequence 18118, A
20	98.5	9.1	821	10	US-09-996-634-62	Sequence 62, Appli
21	98.5	9.1	821	11	US-09-997-182-62	Sequence 62, Appli
22	98.5	9.1	821	11	US-09-997-181-62	Sequence 62, Appli
23	97.5	9.0	2658	9	US-09-815-242-4035	Sequence 4035, Ap
24	97.5	9.0	3285	10	US-09-712-363-143	Sequence 143, App
25	96	8.8	1980	12	US-10-369-493-31940	Sequence 31940, A
26	96	8.8	3331	8	US-08-754-311B-1	Sequence 1, Appli
27	95.5	8.8	599	13	US-10-029-386-20712	Sequence 20712, A
28	95.5	8.8	1317	12	US-10-369-483-11645	Sequence 31645, A
29	95.5	8.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
30	94.5	8.7	389	13	US-10-029-366-13913	Sequence 13913, A
31	94.5	8.7	563	13	US-10-029-366-206	Sequence 206, App
32	94.5	8.7	3044	12	US-10-108-260A-2049	Sequence 2049, App
33	94	8.7	657	10	US-09-974-300-1655	Sequence 1655, App
34	93.5	8.6	594	13	US-10-120-988-71	Sequence 71, Appli
35	93	8.6	2076	15	US-10-156-761-1099	Sequence 7059, App
36	92.5	8.5	699	13	US-10-027-632-24830	Sequence 24830, A
37	92.5	8.5	699	13	US-10-027-632-24831	Sequence 24831, A
38	92.5	8.5	699	13	US-10-027-632-24832	Sequence 24832, A
39	92.5	8.5	699	14	US-10-027-632-24830	Sequence 24830, A
40	92.5	8.5	699	14	US-10-027-632-24831	Sequence 24831, A
41	92.5	8.5	699	14	US-10-027-632-24832	Sequence 24832, A
42	92.5	8.5	1622	13	US-10-029-386-22666	Sequence 22666, A
43	92.5	8.5	2273	10	US-09-882-830A-410	Sequence 410, App
44	92.5	8.5	2390	10	US-09-880-107-3769	Sequence 3769, App
45	92.5	8.5	2390	13	US-09-873-319-717	Sequence 717, App

ALIGNMENTS

RESULT 1
US-09-809-545A-1
Sequence 1, Application US/09809545A
Patent No. US20020110804A1
GENERAL INFORMATION:
APPLICANT: Stanton, Lawrence W.
TITLE OF INVENTION: SECRETED FACTORS
FILE REFERENCE: SCIOS.017A
CURRENT APPLICATION NUMBER: US/09/809,545A
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1340
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-809-545A-1

Alignment Scores:
Pred. No.: 1,82e-118
Score: 1086.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Length: 1340
Matches: 203
Conservative: 0
Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-809-545A-2 (1-203) x US-09-809-545A-1 (1-1340)
 QY 1 MetThrAsnLysValAlaValAsnProTyrThrAsnGlyTPrLysLeuAsnProValVal 20
 535 ATGACATAATAAAGCCCGTGAACCCCTACCAAGGCTGGAATTAATTAATCCAGTTGTG 594
 QY 21 GYAlAValAlTyrSerProAspPheTyrAlaGlyThrValLeuLeuCyseGlnAlaAsnGln 40
 595 GGCCTGCTCAACACCCCGGACTTCTATGACAGGACGGGTGCTGTCAGGCCAACAG 654
 QY 41 GlnGlySerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
 655 GAGGATCTTCCATGTCAGTGAAGGCCCAAGTTCACTTGTATTAATCTTTCGCAATCCCTG 714
 QY 61 PheProTyrProAlaAlaThrAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
 715 TTTCATATCCGCGCCGACCTGTCAGCTGATACGAGGGGCTCACTTCGAGGCCGT 774
 QY 81 GYArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProLleProAlaTyr 100
 775 GGTGCAACCGTGAACAACCTTCAGAGCTGGCGGCCGCCCAATCCCGCCTAT 834
 QY 101 GYValValValTyrGlnGluProValTyrGlyAsnLysLeuGlnGlyGlyTyrAla 120
 835 GCGGAGTAGTGTATCAAGACCGAGTATAGCAATTAATGCTACAGGGGTGACGCT 894
 QY 121 AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaTyrSerAspSerTyrGly 140
 895 GCATACCGCTACGCGCCAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
 QY 141 ArgValTyrAlaAlaAspProTyrHisThrLeuAlaProAlaProThrTyrGlyVal 160
 955 CGAATTATGCTGCGACCCCTACACCAACACTTGTCTCCAGCCCACTACGAGGCTT 1014
 QY 161 GYAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrAspSerHisAlaAspAsp 180
 1015 GGTCCATGAAATGCTTTTGGCCCTTGACGATGCCAAGACTAGAGCCATGCTGATGAT 1074
 QY 181 ValGlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPhe 200
 1075 GTGGGTCTCGTTCTTTCTTCAATTCAGGCTAGTATATACCAAGGGGATACACCGTTT 1134
 QY 201 AlaProTyr 203
 1135 GCTCCATAT 1143
 DB 1135 GCTCCATAT 1143
 RESULT 2
 US-09-794-591-1
 ; Sequence 1, Application US/09794591
 ; Patent No. US20010018198A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pulec, Stefan M.
 ; APPLICANT: Shibata, Hiroki
 ; TITLE OR INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins.
 ; FILE REFERENCE: CE 3093
 ; CURRENT APPLICATION NUMBER: US/09/794,591
 ; PRIOR FILING DATE: 2001-02-26
 ; PRIOR APPLICATION NUMBER: 09/145,391
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 2372
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (987) .. (1979)
 ; US-09-794-591-1

Alignment Scores:
 Pred. No.: 1,136-102 Length: 2372
 Score: 955.00 Matches: 189
 Percent Similarity: 86.94% Conservative: 4
 Best Local Similarity: 85.14% Mismatches: 9
 Query Match: 87.94% Indels: 21
 DB: 9 Gaps: 2
 US-09-809-545A-2 (1-203) x US-09-794-591-1 (1-2372)
 QY 1 MetThrAsnLysValAlaValAsnProTyrThrAsnGlyTPrLysLeuAsnProValVal 20
 1572 ATGACATAATAAAGCCCGTGAACCCCTACCAAGGCTGGAATTAATTAATCCAGTTGTG 1631
 QY 21 GYAlAValAlTyrSerProAspPheTyrAlaGlyThrValLeuLeuCyseGlnAlaAsnGln 40
 1632 GGTGAGTCTTCCATGTCAGTGAAGGCCCAAGTTCACTTGTATTAATCTTTCGCAATCCCTG 1691
 QY 41 GlnGlySerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
 1692 GAGGATCTTCCATGTCAGTGAAGGCCCAAGTTCACTTGTATTAATCTTTCGCAATCCCTG 1751
 QY 61 PheProTyrProAlaAlaThrAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
 1752 TTCCCGTATCCAGACGACCCGCGCGCCCTTACCGAGGGGCGACCTGCGAGGCCGC 1811
 QY 81 GYArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProLleProAlaTyr 100
 1812 GGTGCAACCGTGAACAACCTTCAGAGCTGGCGGCCGCCCAATCCCGCCTAT 1871
 QY 101 GYValValValTyrGlnGluProValTyrGlyAsnLysLeuGlnGlyGlyTyrAla 120
 1872 GCGGAGTAGTGTATCAAGACCGAGTATAGCAATTAATGCTACAGGGGTGACGCT 1928
 QY 120 AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaTyrSerAspSer----- 138
 1929 TGCATACCGCTACGCGCCAGCTACCCCTGCACTGCGCTGCTACAGTACAG-AAATC 1987
 QY 139 -----TyrGlyArgVa 142
 1988 AGTTCGCTTCTTTCGACGACGATGAATTTCTTGAACACTTGCACGTTACGAGCAGT 2047
 QY 142 TTYAlaAlaAspProTyrHisThrLeuAlaProAlaProThrTyrGlyValGlyAl 162
 2048 TTATGCTGCCGACCCCTACACCAACGACTTGTCTCAAGCCCACTACGCGGTGTC 2107
 QY 162 aMetAsnAlaPheAlaProLeuThrAspAlaLysThrAspSerHisAlaAspAspValG 182
 2108 CATGAATGCTTTGCACTTGAATGCTGACGACGACGACGACGACGACGACGACGACGACG 2167
 QY 182 YLeuValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPheAlaP 202
 2168 TCTGCTTCTTCTTCAATTCAGGCTAGTATATACCGAGGGGATACACCGCTTTTGTCTCC 2227
 QY 202 QTYr 203
 2228 ATAC 2231
 DB 2228 ATAC 2231
 RESULT 3
 US-10-094-749-287
 ; Sequence 287, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUJI
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI

APPLICANT: OTSUKA, KAORU
 APPLICANT: NAGAI, KEIICHI
 APPLICANT: IRIE, RYOTARO
 APPLICANT: TAMECHIKI, ICHIRO
 APPLICANT: SEKI, NAOHICO
 APPLICANT: YOSHIKAWA, TSUTOMU
 APPLICANT: OTSUKA, MOTOFUKI
 APPLICANT: NAGAHARI, KENJI
 APPLICANT: MASUHO, YASUHIKO
 TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
 FILE REFERENCE: 084335/0160
 CURRENT APPLICATION NUMBER: US/10/094,749
 CURRENT FILING DATE: 2002-03-12
 PRIOR APPLICATION NUMBER: 60/350,435
 PRIOR FILING DATE: 2002-01-24
 PRIOR APPLICATION NUMBER: JP 2001-328381
 PRIOR FILING DATE: 2001-09-14
 NUMBER OF SEQ ID NOS: 3381
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 287
 LENGTH: 1558
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-094-749-287

Alignment Scores:
 Pred. No.: 2,04e-51 Length: 1558
 Score: 519.00 Matches: 119
 Percent Similarity: 59.64% Conservative: 14
 Best Local Similarity: 53.36% Mismatches: 39
 Query Match: 47.79% Indels: 52
 DB: 13 Gaps: 8

US-09-809-545a-2 (1-203) x US-10-094-749-287 (1-1558)

QY 1 MetThrAsnLysAlaValAsnProTyrrThraSngLYTrrLysLeuAnProValVal 20
 DB 854 ATGACCAATGAAGATGTCACACCATATGTAAGTAATTAAGCCAGTAGTT 913
 QY 21 GYAlaValTyrrSerProAspPheTyrrAla----- 30
 DB 914 GAGCGTGTATATGTCGAGTATATATGACATTCAGCTTCAAGCAGATGTGCTTA 973
 QY 31 GYThr-ValLeuLeuCySGlnAlaEngInglYSerSerMetTyrrSerGlyProse 50
 DB 974 GCGAATGATGACAGAGTCCCTATCGAAGAGGGGTATCAACACTTACATT-CCT-- 1030
 QY 50 rSerLeuValTyrrThraSerAlaMetProGlyPheProTyrrPro--AlaAlaThrAlaAl 69
 DB 1031 ---TTATCATGCTCCCTTATGTTCTGCTTCCCTTACCTATGACGACGACGACGCG 1086
 QY 69 aAlaAlaTyrrArgLYAlaAlaHisLeuArgLYArgLYArgLYValTyrrAsnThrPheAr 89
 DB 1087 AGCGCGCTTTCAGAGAGCCATTGAGGGGCGACAGGGCGAGCATATATGTCAGTCCG 1146
 QY 89 gAlaAlaAlaProProProProProProProProProProProProProProProProPro 109
 DB 1147 A---GGCGTACCTTCCACAGCCATCCCGCTTACAGGTGTGTTTACAGAGCGGATT 1203
 QY 109 lYrGlyAsnLysLeuLeuEngInglYrAlaAlaTyrrArgLYArgLYArgLYProThrPr 129
 DB 1204 TTAAGGTCGTAC---CTTATGTGTGATATGACGCTTACAGATATGACAGCTGTAC 1260
 QY 129 cAlaThr-----AlaAlaAlaTyrrSerAspSerTyrrGlyAr 141
 DB 1261 TGAACCGCAGCAGCCGCTGTCAGCCGCTGACGCGCTTACGATGACGCTTATGCGAG 1320
 QY 141 gValTYrrAlaAlaAspProTyrrHisThrLeuAlaProAlaProThrTyrrGlyValG 161
 DB 1321 GGGTATACAGCGGACCCCTTAC---CATGCCCTTGCCCTGCGGCTTACGTATGAGTTGG 1377
 QY 161 yAlaMetAsnAlaPheAlaProLeuThrAspAlaTyrrArgSerHisAlaAspAspVa 181

DB 1378 CGCTGTG----- 1384
 QY 181 lGlyLeuValLeuSerSerLeuGlnAlaSerIleTyrrGlnGlyTYrrAsnArpPheAl 201
 DB 1385 -----CCGAGTTTATACCAAGGTGCTTACAGCGATTTC 1419
 QY 201 aProTyrr 203
 DB 1420 CCCCTAC 1426

RESULT 4

US-09-919-039-266
 Sequence 266, Application US/09919039
 Publication No. US20030108871A1
 GENERAL INFORMATION:
 APPLICANT: Kaser, Matthew R.
 TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 FILE REFERENCE: PA-0035 US
 CURRENT APPLICATION NUMBER: US/09/919,039
 CURRENT FILING DATE: 2002-09-09
 PRIOR APPLICATION NUMBER: 60/222,113
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 401
 SOFTWARE: PERL Program
 SEQ ID NO 266
 LENGTH: 1843
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 OTHER INFORMATION: Incyte ID No. US20030108871A1 253783.3
 FEATURE:
 NAME/KEY: unsure
 LOCATION: 1824
 OTHER INFORMATION: a, t, c, g, or other
 US-09-919-039-266

Alignment Scores:
 Pred. No.: 3.89e-49 Length: 1843
 Score: 500.50 Matches: 105
 Percent Similarity: 52.61% Conservative: 6
 Best Local Similarity: 49.76% Mismatches: 23
 Query Match: 46.09% Indels: 77
 DB: 11 Gaps: 5

US-09-809-545a-2 (1-203) x US-09-919-039-266 (1-1843)

QY 1 MetThrAsnLysAlaValAsnProTyrrThraSngLYTrrLysLeuAnProValVal 20
 DB 1228 ATGACCAACAGAGAGCGGGAACCCCTTACACCAACGCTGAGACTAATCCAGTGTGTC 1287
 QY 21 GYAlaValTyrrSerProAspPheTyrrAlaGlyThrValLeuLeuCySGlnAlaEngIn 40
 DB 1288 GCGCGAGCTTACAGGGCGCTGAATTCTATATGACGTGACG----- 1323
 QY 41 GluGlySerSerMetTyrrSerGlyProSerSerLeuValTyrrThraSerAlaMetProGly 60
 DB 1324 -----GGG 1326
 QY 61 PheProTyrrProAlaAlaThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 80
 DB 1327 TTCCTTATCCACACACCGGACAGCCGCTGCTTACCGGGGCGACATCTTCCGGGCGCG 1386
 QY 81 GYArgThrValTyrrAsnThrPheArgAlaAlaAlaAlaProProProProProProPro 100
 DB 1387 GCGCGGCGGTATATATATATATGCTTGGCGGCGACCCCGACCCCGCATCCGACTTAC 1446
 QY 101 GYGlyLY----- 102
 DB 1447 GAGCGGACACTGAGCAAAACGCTTGTAAATGCAATGCCATGGGCGGCGCTGCGACCG 1506
 QY 102 ----- 102

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Db      1507 TGCCCCCTCCCTCCTCAGACAGACCGGAGCGGCTTACCCACTCTCCAGCGCTTCCA 1566
Qy      103 -----ValValTyrGlnGluProValTyrGlyAsnLys 113
Db      1567 CCACCTTCTGTCGCTTGTCTCCAGGAGTCTGTATCAGATGGATTATTGGTGTGAG 1626
Qy      114 LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThrAlaAla 133
      1627 ---ATTATGAGGCTACGACGAGCTTACAGATAGCTCAGCCCGCT---GCAGCGGCGCA 1680
Db      134 AlaTyrSerAspSerTyrGlyArgValTyr---AlaAlaAspProTyrHisThrLeu 152
      1681 GCCTACAGCAGCAGATTACGAGAGAGTCTACGACGCTCCGACCGCTACATCACACATC 1740
Qy      153 AlaProAlaProThrTyrGlyValGlyAlaMet 163
Db      1741 GGGCGCGGCGGACCTTACAGCATTGGAAACATG 1773

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RESULT 5

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US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIORITY FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIORITY FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 1250374
US-10-359-385-5

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Alignment Scores:
Pred. No.: 2,37e-45 Length: 1506
Score: 467.50 Matches: 107
Percent Similarity: 56.48% Conservative: 15
Best Local Similarity: 49.54% Mismatches: 39
Query Match: 43.05% Indels: 56
DB: 13 Gaps: 8

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US-09-809-545a-2 (1-203) x US-10-359-385-5 (1-1506)

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Qy      1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTyrLysLeuAsnProValVal 20
      768 ATGACCAATAGAGAGATGCTACACCATATCAATGCTTGAATTAAGCCGCTACT 827
Db      21 G1yAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCySglnAlaAsn--- 39
      828 GGAAGCTGATATGTCGCGAGTATATGACAGCATCCAGCTTCAAGAGATGTCTCCTA 887
Qy      40 ---GlnGluGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
      888 GGCATATGATGACAGAGCCCTTATCAGGAAGAGGGGTATCAACACTTACATTCTTTA 947
Qy      57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
      948 ATCATCTCTGCTTCTTACCTTACCTGACGACACGACGACGCGCTTTCAGAGAGCC 1007
Db      76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95

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Db      1008 CATTTGAGGGGAGAGGGGCGGACGATATATGTGACGTCCGA---GCGTACCTCCAAACA 1064
Qy      96 ProIleProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAsnLysLeuLeu 115
Db      1065 GCATCTCCCGCCCTATCC----- 1081
Qy      116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
      1082 AGGGGTGATATGACACTTACAGATATGACACAGCCGTCTACTCCAACCGGACCGCT 1141
Db      132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
      1142 GCTGACCGCGCTGACCGCTTACAGTACGATGAGGTTATGCGAGGTGTACACAGCCGCC 1201
Qy      148 TyrHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
      1202 TAC---CATGCCCTTGTCCCTGCGCTGAGCTATGAGATTGGCCCTGTG----- 1246
Qy      168 ProLeuThrAspAlaTyrThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
      1246 ----- 1246
Qy      188 LeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPheAlaProTyr 203
      1247 -----GCGAGTTTATACGAGGTGGCTACAGCCGATTGGCCCCCTTAC 1288

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RESULT 6

```

US-10-104-047-659
; Sequence 659, Application US/10104047
; Publication No. US2003023632A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US2003023632A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIORITY FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 659
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-659

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Alignment Scores:
Pred. No.: 3,22e-17 Length: 2397
Score: 231.50 Matches: 51
Percent Similarity: 57.00% Conservative: 6
Best Local Similarity: 51.00% Mismatches: 8
Query Match: 21.32% Indels: 35
DB: 12 Gaps: 3

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US-09-809-545a-2 (1-203) x US-10-104-047-659 (1-2397)

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Qy      112 AsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
      2058 TCTTCTCTCTGTATGAGGTGATATGACGCTTACAGATATGACAGCTGTACTGCAACC 2117
Db      132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyr 143
      2118 GAGACGACCGCTGTCGACGCGCTTACAGTATGACGATTATGACAGGGGTGTAC 2177
Qy      144 AlaAlaAspProTyrHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMet 163
      2178 ACAGCCGACCCCTTAC---CATGCCCTTGTCCCTGCGCTGAGCTATGAGATTGGCGCTGTG 2234
Qy      164 AsnAlaPheAlaProLeuThrAspAlaTyrThrArgSerHisAlaAspAspValGlyLeu 183
      2234 ----- 2234
Db      184 ValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPheAlaProTyr 203

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Db 2235 -----GCAGCTTATACCGAGGTGGCTAACGCCCATTTGGCCCCCTAC 2276

RESULT 7

US-10-301-822-25

Sequence 25, Application US/10301822

Publication No. US20030148410A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Berger, Allison

APPLICANT: Guillemette, Tracy L.

APPLICANT: Kamatkar, Shubhangi

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Burgart, Lawrence J.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

FILE REFERENCE: MEM01-029P2RNM

CURRENT APPLICATION NUMBER: US/10/301,822

PRIOR FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/339,971

PRIOR FILING DATE: 2001-12-10

PRIOR APPLICATION NUMBER: US 60/361,978

PRIOR FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 60/381,988

PRIOR FILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 25

LENGTH: 11447

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(9192)

US-10-301-822-25

Alignment Scores:

Pred. No.: 0.0107 Length: 11447

Score: 116.00 Matches: 45

Percent Similarity: 34.08% Conservative: 16

Best Local Similarity: 25.14% Mismatches: 54

Query Match: 10.68% Indels: 64

DB: 13 Gaps: 8

US-09-809-545a-2 (1-203) x US-10-301-822-25 (1-11447)

Qy 50 SerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAla 69

Db 6232 AACAAATGTAATCTGACGCCCTGCAACCTGACACTCTCATAT--AAATTTACTGTATT 6288

Qy 70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyTyrArgTyrAla----- 84

Db 6289 GCTGTTATATGAAGTGAAGTGAAGTGGCCATCTTAACGGAATGGAAGAACTGGGGAGCTC 6348

Qy 85 -----TyrAsnThrPheArgAlaAlaAla 92

Db 6349 CTTCTCTCGAACAATACATCTCTGACGAATGGATATCAAGATTCAAGGTGCTCTCG 6408

Qy 93 ProProProProLeuProAlaTyrGlyGlyValValTyrGlnGlnProValTyrGlyAsn 112

Db 6409 GATCTCTTACCTCTTCCAGTCTTGGATATAAATGATATAAGCCAGTGGCTTCCAAAT 6468

Qy 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro 129

Db 6469 GAGCCCATGGAAGCCTTGTGGGAAATGACATCATATCCTTA----- 6513

Qy 130 AlaThrAlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspProTyrHis 149

Db 6513 ----- 6513

Qy 150 HisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla----- 167

Db 6514 CACAACTCAATCCCAAGCAACCTTACGATGTG-----AATGTTATGCTCAATAT 6564

Qy 168 -----ProLeuThrAspAlaLysThrArgSerHisAlaAspVal 181

Db 6565 GATTCGTGACAGTGTCTCCCTTGACGATCAAGGCACTTACA----- 6606

Qy 182 GlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPhe 200

Db 6607 ---TTATATTTAATGTAACAGATCTGAATAACTTACCAAGTTGGTGGATATCATTC 6660

RESULT 8

US-10-177-293-60

Sequence 60, Application US/10177293

Publication No. US20030124128A1

GENERAL INFORMATION:

APPLICANT: Lillie, James

APPLICANT: Glat, Karen

APPLICANT: Zhao, Xumei

APPLICANT: Ganavarpu, Manjula

APPLICANT: Kamatkar, Shubhangi

APPLICANT: Mertens, Maureen

APPLICANT: Meyer, Vic

APPLICANT: Wang, Youzhen

APPLICANT: Xu, Yongyao

APPLICANT: Hoersch, Sebastian

APPLICANT: Monahan, John

APPLICANT: Meyers, Rachel E.

APPLICANT: Bast Jr., Robert C.

APPLICANT: Hortobagyi, Gabriel N.

APPLICANT: Pusztai, Lajos

APPLICANT: Meric, Funda

APPLICANT: Sahin, Aysegul

APPLICANT: Mills, Gordon B.

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,

TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER

FILE REFERENCE: MRI-038

CURRENT APPLICATION NUMBER: US/10/177,293

PRIOR FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US 60/299,887

PRIOR FILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: US 60/301,572

PRIOR FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: US 60/306,501

PRIOR FILING DATE: 2001-07-18

PRIOR APPLICATION NUMBER: US 60/325,002

PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US 60/362,585

PRIOR FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 60/xxx,xxx

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 506

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 60

LENGTH: 11447

TYPE: DNA

ORGANISM: Homo sapiens

US-10-177-293-60

Alignment Scores:

Pred. No.: 0.0107 Length: 11447

Score: 116.00 Matches: 45

Percent Similarity: 34.08% Conservative: 16

Best Local Similarity: 25.14% Mismatches: 54

Query Match: 10.68% Indels: 64

DB: 15 Gaps: 8

US-09-809-545a-2 (1-203) x US-10-177-293-60 (1-11447)

Qy 50 SerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAla 69

Db 6232 AACAAATGTAATCTGACGCCCTGCAACCTGACACTCTCATAT--AAATTTACTGTATT 6288


```

PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11039
LENGTH: 11657
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc_feature
LOCATION: 1, 2, 3, 4, 11656, 11657
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11039

Alignment Scores:
Pred. No.:      0.0109      Length:      11657
Score:          116.00      Matches:     45
Percent Similarity: 34.08%   Conservative: 16
Best Local Similarity: 25.14% Mismatches:    54
Query Match:      10.68%     Indels:       64
DB:              15         Gaps:         8

US-09-809-545A-2 (1-203) x US-10-198-846-11039 (1-11657)

QY      50 SerSerLeuValIyThrThrSerAlaMetProGlyPheProTyrrProAlaAlaThrAlaLa 69
        : ::::: ||| |
Db      6398 AACATGTAAATACGTGCAGCCCTCGTCAMCCTGCACACTCATAT--AAATTACTTTATT 6454A
QY      70 AlaAlaIyTfArg-----GlyAlaHisLeuArGgiYArGgiYArGThrVal----- 84
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      6455 GCTGTTTGAAGATGAGATGGTGCCATCTAACAGAAATGAGAAGACTGTGGACTC 6514T
QY      85 -----TyrAenThrPheArGAlaAlaLa 92
        : ::::: ||| |
Db      6515 CTTCCTCTCAGACATACATCTCTGACGAATGTATTAACAAGATTCAAGGATGCTCG 6574A
QY      93 ProProProProlleProAlaIyGlyIyValIyTrgInuProValIyTrGIyAsn 112
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      6575 GATCCCTCACCTTCTCCAGTTCTTGGAATATAAATAGATATAAAGCCAGTGGGCCAAT 6634A
QY      113 LysLeuLeuGln-----GlyGlyTyrAlaAlaIyTfArgTyrrAlaGlnProThrPro 129
        : ::::: ||| |
Db      6635 GAGCCCATGAGAGCCCTTTGTTGGAGAAATGACATATATACCTTA----- 6679A
QY      130 AlaThrAlaAlaAlaIySerAspSerTyrrGlyArGValTyrAlaAlaAspProTyxHis 149
        : ::::: ||| |
Db      6679 ----- 6679A
QY      150 HisThrIleuAlaProAlaProThrTyrrGlyValGlyAlaMetAsnAlaPheAla---- 167
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      6680 CACAAATCATATCCAGCACACACCCTACCATGTG-----AATGTTTAGTCCATATAT 6730A
QY      168 -----ProLeuThrAspAlaIyStrHArGSerHisAlaAspAspVal 181
        : ::::: ||| |
Db      6731 GATTCTGCACTCAAGTGTCCCCTTGACAAATCAAGGCACTACA----- 6772A
QY      182 GlyLeuValLeuSerSerLeuGlnAlaSerIleTyrrGlnGlyIyTyrAsnArGphe 200
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      6773 ---TTATATTTAATGTAAACAGACTGTGA AAAAATTACAGCAATTGGGTGGGATACATTC 6826

RESULT 11
US-10-098-841-226
; Sequence 226, Application US/10098841
; Publication No. US20020197679A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunding
APPLICANT: Wang, DianRui
APPLICANT: Zhao, Qing A.
```

	APPLICANT:	Ren, Feiyan	
	APPLICANT:	Chen, Rui-hong	
	APPLICANT:	Wang, Dunrui	
	APPLICANT:	Wang, Zhiwei	
	APPLICANT:	Wehrman, Tom	
	APPLICANT:	Zhang, Jie	
	APPLICANT:	Olan, Xiaohong B.	
	APPLICANT:	Dmanac, Radje T	
	TITLE OF INVENTION:	No. US20020197679A1el Nucleic Acids and Peptides	
	FILE REFERENCE:	784CIP2	
	CURRENT APPLICATION NUMBER:	US/10/098,841	
	PRIOR FILING DATE:	2002-03-13	
	PRIOR APPLICATION NUMBER:	09/598,042	
	PRIOR FILING DATE:	2000-06-20	
	PRIOR APPLICATION NUMBER:	09/552,317	
	PRIOR FILING DATE:	2000-04-25	
	PRIOR APPLICATION NUMBER:	09/488,725	
	PRIOR FILING DATE:	2000-01-21	
	NUMBER OF SEQ ID NOS:	331	
	SOFTWARE:	pc FL_genes Version 1.0	
	SEQ ID NO 226		
	LENGTH:	6930	
	TYPE:	DNA	
	ORGANISM:	Homo sapiens	
	FEATURE:		
	NAME/KEY:	CDS	
	LOCATION:	(234) ..(968)	
	US-10-098-841-226		
	Alignment Scores:		
	Pred. No.:	0.0429	Length: 6930
	Score:	108.50	Matches: 56
	Percent Similarity:	35.85%	Conservative: 20
	Best Local Similarity:	26.42%	Mismatches: 67
	Query Match:	9.99%	Indels: 69
	DB:	14	Gaps: 12
US-09-809-545A-2 (1-203) x US-10-098-841-226 (1-6930)			
QY	6	AAlaValAsnProTyrThrAsnGlyTrpIysLeuAsnProValAGlAlaValTyrSer	25
DB	336	GCCTACCAATCCC-----ACCCTGRACCCACCAAATAGTCACATTATGCT	380
QY	26	ProAspPhe-----TyrAlaGlyThrValLeuLeuCysGlnAlaAsn	39
DB	381	CCAGAATTTCAGTTCTCTCGCATTCACACTTATGCA--ACTCGTGAGTAAGAACGGCTCG	437
QY	40	GInGluGlySerSer-----MetTyrSerGly	48
DB	438	CCACAAGAACTCGCTTCCTGTGGCAGTAGAAGGACCTTCCACTCCAGTGGACACCGGG	497
QY	49	ProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaIleThra	68
DB	498	ACCGAGAACCGAACTTACCAAGCACATCTCTGGCGCTTCAGATAT-----ACTGCC	548
QY	69	AlAlaAlaIleTyrArgGlyValHisIleuArgGlyArgThrValTyrAsnThrPhe	88
DB	549	GGGACACCACTACAG-----GTCCACACGACCCAG	578
QY	89	ArgAlaAlaIleProProProProIleProAlaTyrGlyGlyValTyrGInGluPro	108
DB	579	AGTAAACACTGCTCCACCCCCCTACTCCCATCACCACAAAC-----CCCTATCAGACGGCC	632
QY	109	ValTyr-----GlyAsnIysLeuLeuGInGlyTyrAla	120
DB	633	ATGTATATCCAATCAGAAGTGCCTACCCCAAGCAAGATCTGTATGCCACGGAGGCTTAC--	689
QY	121	AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaIleTyrSerAspSerTyrGly	140
DB	690	-----TACACACACGGC-----	701
QY	141	ArgValTyrAlaIleAspProTyr-----HisHisThrIleuAlaProAlaProThrTyr	158

```
Db 702 ---GTGATGTCGCCGACCTCATGTCACACACGAGTCTCCAGCCCAAC--- 755
|||
Qy 159 G1yValG1yAlaMetAlaPheAlaProLeuThrAspAlaIleThrArgSerHisAla 178
|||
Db 756 ---AGCATCTCCCTGCTATCTTACCCAGACCTTGTGCGCCGAGAGACCAACGCT 809
|||
Qy 179 AspApeValG1yLeuValIleuSerSerLeuGlnAla 190
|||
Db 810 GTGCCCATGGGCGATGGTCAGCAGCAGCACCACCATGGCA 845

RESULT 12
US-09-770-445-481/C
; Sequence 481, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Goflach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hubban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: PaacSeq for Windows Version 4.0
; SEQ ID NO 481
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-481

Alignment Scores:
Pred. No.: 0.00456 Length: 895
Score: 107.00 Matches: 52
Percent Similarity: 36.60% Conservative: 19
Best Local Similarity: 26.80% Mismatches: 63
Query Match: 9.85% Indels: 60
DB: Gaps: 11

US-09-809-545A-2 (1-203) x US-09-770-445-481 (1-895)
Qy 42 G1ySerSerMetTyRserG1yProSerSerLeuValTyThrSerAlaMetProG1yPhe 61
|||
Db 869 GGTATATGTCCTTACCAAGTCCA-----ACACGACGACGACCGTCATAT 825
|||
Qy 62 ---ProTyRProAlaIle-----ThraAlaIleAlaIleTyArgG1yAla 75
|||
Db 824 GATTCAACACGACGACGATCGATGTTCAACTCAGCAGCAGCATCGTATGTTCA 765
|||
Qy 76 HisLeuArgG1yArg-----G1yArgThrValTyR 85
|||
Db 764 AACCTGGCTCAACACACCAATATGTTATGATCATCAAGTGGCGCTACTACCAAACTTAT 705
|||
Qy 86 AsnThrPheArgAlaIleAlaPro-----ProProProIle 97
```

```
Db 704 CCTTCATATAGCTCTCCAGACCATCATGTTATATGTTACACAAACCCAGCAGTT 645
|||
Qy 98 ---ProAlaTyR-----G1yG1yValValTyRIng1uPro 108
|||
Db 644 GCCCCAGCTTATATAGCAGCAGCAGGTGCTCAGCCAGCTTCGTGTGCAACAAACTTACGT 585
|||
Qy 109 ValTyRGlYAsnLysLeuLeuGlnG1yTyRAlaAlaTyRArgTyRAlaGlnProThr 128
|||
Db 584 GGGTACGGGGAAGTACTCCCAACCGGTGCTATAGTTCATCTCCACACAGCGCGCT 525
|||
Qy 129 ProAlaThrAlaIleAlaIleTySerAsp---SerTyRGlYArgValTyRAlaIleAspPro 147
|||
Db 524 TATGTATATACCCCGCTCAACAGCATGAAACTATGGA-----TACATTGGCTCTCAG 471
|||
Qy 148 TyRHisIleThrLeuAlaProAlaProThrTyRGlYValG1yAlaMetAsnAlaPheAla 167
|||
Db 470 TAT-----CCTAGCTATGAGAGTGGAAGCAGCATCAGCATATGCT 432
|||
Qy 168 ProLeuThrAspAlaIleTyRThrArgSerHisAlaAspApeValG1yLeuValIleuSerSer 187
|||
Db 431 GCACCTACTGCGCAACCGCTTATTC-----TACATTGGCTCTCAG 405
|||
Qy 188 LeuGlnAlaSerIleTyRIng1yG1yTyRAsnArgPheAla 201
|||
Db 404 ---CAGACTGCACCTCTCTCAGCGCGCTATGACCAATCAGCA 366
|||

RESULT 13
US-10-252-157-219
; Sequence 219, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Pearson, Cecelia I.
; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: PA-0027-1 US
; CURRENT APPLICATION NUMBER: US/10/252,157
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,048
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: PERL Program
; SEQ ID NO 219
; LENGTH: 7053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030190640A1 354430.4
; NAME/KEY: unsure
; LOCATION: 727, 736, 1204, 1985-2065, 3071-3101, 6410, 6426, 6429, 6432, 6441, 6450,
; LOCATION: 6772
; OTHER INFORMATION: a, t, c, g, or other
US-10-252-157-219

Alignment Scores:
Pred. No.: 0.196 Length: 7053
Score: 103.00 Matches: 52
Percent Similarity: 36.00% Conservative: 20
Best Local Similarity: 26.00% Mismatches: 64
Query Match: 9.48% Indels: 64
DB: Gaps: 11

US-09-809-545A-2 (1-203) x US-10-252-157-219 (1-7053)
Qy 18 ProValValG1yAlaValTyRserProAspPhe-----TyRAlaG1y 31
|||
Db 159 CCCACCAATATGTCCTCAAGTATGCTCCAGAGTTTCAGTCTCGATTCAGCTTATGCA--- 215
|||
Qy 32 ThrValLeuLeuG1ySerGlnAlaGlnGlnG1ySer----- 44
|||
Db 216 ACTCTGCTATGAAGACAGGCTGCGCACAGAACTGCTTCTGCTGCACTGAAGGACCC 275
```

```

Qy 45 -----MetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
Db 276 TTCACCTCCAGTGGACACCGGAGACCGAAGCACTTACCAAGCATCTCTGGGGCT 335
Qy 61 PheProTyrProAlaAlaThrAlaAlaAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyAsp 80
Db 336 TTCCAGATAT-----ACTGGGGGACACCATACAG----- 365
Qy 81 GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProleProAlaTyr 100
Db 366 -----GTCCACCGACCGACAGATTAACATGCTCTACCCCTCTACTCCCATGACCC 416
Qy 101 GlyGlyValValTyrGlnGluProValTyr-----GlyAsn 112
Db 417 AAC-----CCCATATGACGAGCGCATCTATCCATGAGAGTGCCTTACCCCGACAGAA 470
Qy 113 LysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThrAla 132
Db 471 CTGTATGCCAGGAGGAGCTTAC-----TACACACAGCCG----- 503
Qy 133 AlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspProTyr-----HisHis 150
Db 504 -----GTGTATGCTGCCAGCCTCATGTCTATCCATCCACAT 536
Qy 151 ThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAlaProLeuThr 170
Db 537 ACCACGCTCTCCAGCCCAAC-----AGCATTCCTCTCTGTATCTATCCAGACACT 587
Qy 171 AspAlaLysThrArgSerHisAlaAspAspValGlyLeuValLeuSerSerLeuGlnAla 190
Db 588 GTTGCCGCGCCGAGACCAAGGTGTGGCATGGGAGTGTGGAGGACACCACTGAGCA 647

```

RESULT 14

```

US-10-156-761-2655
; Sequence 2655, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 2655
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1089)
US-10-156-761-2655

```

Alignment Scores:

```

Pred. No.: 0.02 Length: 1089
Score: 102.50 Matches: 48
Percent Similarity: 40.00% Conservative: 18
Best Local Similarity: 29.09% Mismatches: 55
Query Match: 9.44% Indels: 44
DB: 15 Gaps: 10

```

US-09-809-545a-2 (1-203) x US-10-156-761-2655 (1-1089)

```

Qy 59 ProGlyPheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgGlyAlaHisLeuArg 78
Db 636 CCTGGGCGCCCTACAGACGACGAAAGCCCTTCCAGACACGACGAGCGCGACTACTCT 695
Qy 79 GlyArgGly-ArgThrValTyrAsnThr---PheArgAlaAlaAlaProPro----- 94
Db 696 GGCCTGCTGGCGGACCTCGGCAACACCCCGACCGCCTTGGGACCGCCCGACAGACCC 755
Qy 95 -----ProProleProAlaTyrGlyValValTyrGlnGluProValTyrGlyAs 112
Db 756 CCAGGCCCTTGAGATCCGGCT-----CACCGCAGTAC----- 789
Qy 112 nLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro----- 129
Db 790 -----GGCGGGCAGAGACGCTTACCGTATCCAGACGAGACCCCGATCCCTTA 836
Qy 130 -----AlaThrAlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAsp 147
Db 837 CGGCTACACGACGACGATACGCGCAGACGAGCGGTACGAGCCGACGCGGACCC 896
Qy 147 CTYrHisHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPhe 166
Db 897 GTAC-----GCCGCTACCCGACGAGGCTACGACGACGAGCGGCTACCA 944
Qy 167 -----AlaProLeuThr---AspAlaLysThrArgSerHis 177
Db 945 CCAGAACGACGACGAGCGCTACTCCACGCGCAGACGACGACTCCACGCGCAGACCA 1004
Qy 177 g---AlaAspAspValGlyLeu-----ValLeuSerSerLeuGlnAlaSerHis 192
Db 1005 CGACCTGGACGAGCGGCGAGCCTCTTCGACACGACGATGACGTGGGAGACGACTCGGAGC 1064
Qy 192 eTyrGlnGlyGly 196
Db 1065 CTACGAAACGGGG 1077

```

RESULT 15

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US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

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Alignment Scores:

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Pred. No.: 2.37e+03 Length: 9025608
Score: 102.50 Matches: 48
Percent Similarity: 40.00% Conservative: 18
Best Local Similarity: 29.09% Mismatches: 55
Query Match: 9.44% Indels: 44

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 15, 2004, 08:41:56 / Search time 67.0883 Seconds
(without alignments)
1335.564 Million cell updates/sec

Title: US-09-809-545A-2

Perfect score: 1086

Sequence: 1 MTNKKAVNPTNGMKLNPPV.....VLSLSQASYYGGYNRFAPY 203

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA_QPWT=fastap -SUFIX=tni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTENT=pico -NOCME=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09809545 @CGN 1.1 133 @runat_15012004_061051_2480 -NCPUS=6 -ICPU=3
-NO_NMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	955	87.9	2372	3	US-09-145-391-1
2	467.5	43.0	1506	4	US-09-176-657-5
3	467.5	43.0	1506	4	US-09-421-299-5
4	101	9.3	914	2	US-08-935-450-10
5	98.5	9.1	821	3	US-08-990-823-62
6	98.5	9.1	821	4	US-09-477-135A-62
7	97.5	9.0	4403765	3	US-09-103-840A-2
8	97.5	9.0	4411529	3	US-09-103-840A-1
9	96	8.8	3231	1	US-08-195-152-1
10	94.5	8.7	4403765	3	US-09-103-840A-2
11	94	8.7	2368	4	US-09-343-011B-3
12	94	8.7	43280	2	US-08-804-227C-1

13	92.5	8.5	2371	2	US-08-343-443B-1	Sequence 1, Appl1
14	92.5	8.5	2412	1	US-08-437-027-18	Sequence 18, Appl1
15	92.5	8.5	28958	1	US-08-258-261B-6	Sequence 6, Appl1
16	92.5	8.5	28958	1	US-08-456-837-6	Sequence 6, Appl1
17	92.5	8.5	28958	1	US-08-457-342-6	Sequence 6, Appl1
18	92.5	8.5	28958	1	US-08-457-646A-6	Sequence 6, Appl1
19	92.5	8.5	28958	1	US-08-458-076A-6	Sequence 6, Appl1
20	92.5	8.5	28958	1	US-08-764-233A-4	Sequence 4, Appl1
21	92.5	8.5	28958	1	US-08-457-335A-6	Sequence 6, Appl1
22	92.5	8.5	28958	1	US-08-729-214-6	Sequence 6, Appl1
23	92.5	8.5	28958	3	US-09-028-934-6	Sequence 6, Appl1
24	92.5	8.5	28958	3	US-08-764-233A-1	Sequence 1, Appl1
25	92	8.5	53526	3	US-08-658-136-2	Sequence 2, Appl1
26	92	8.5	53577	3	US-08-658-136-1	Sequence 1, Appl1
27	91	8.4	1896	4	US-09-343-011B-4	Sequence 4, Appl1
28	90.5	8.3	852	4	US-09-252-991A-16108	Sequence 16108, A
29	90.5	8.3	1311	4	US-09-252-991A-16493	Sequence 16493, A
30	90.5	8.3	10095	3	US-08-822-586-45	Sequence 45, Appl1
31	90	8.3	2303	4	US-09-922-146-3	Sequence 3, Appl1
32	89.5	8.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
33	89	8.2	1083	4	US-09-252-991A-8817	Sequence 8817, Ap
34	89	8.2	1140	3	US-09-023-173-4	Sequence 4, Appl1
35	89	8.2	1227	4	US-09-252-991A-9232	Sequence 9232, Ap
36	89	8.2	1296	4	US-09-252-991A-9150	Sequence 9150, Ap
37	89	8.2	2715	4	US-09-252-991A-8715	Sequence 8715, Ap
38	88.5	8.1	2007	4	US-09-252-991A-3308	Sequence 3308, Ap
39	88.5	8.1	2709	4	US-09-252-991A-3326	Sequence 3326, Ap
40	88	8.1	885	4	US-09-252-991A-4426	Sequence 4426, Ap
41	88	8.1	1362	4	US-09-252-991A-4184	Sequence 4184, Ap
42	88	8.1	2923	6	5187076-5	Patent No. 5187076
43	87.5	8.1	3155	4	US-09-442-100-7	Sequence 7, Appl1
44	87.5	8.1	3155	4	US-08-939-106-7	Sequence 7, Appl1
45	87.5	8.1	44377	2	US-08-804-227C-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-145-391-1
Sequence 1, Application US/09145391
Patent No. 6194171
GENERAL INFORMATION:
APPLICANT: Shihata, Hiroki
TITLE OF INVENTION: Nucleic Acid Encoding Ataxin-2 Binding Proteins,
FILE REFERENCE: CE 3093
CURRENT APPLICATION NUMBER: US/09/145,391
CURRENT FILING DATE: 1998-09-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (987) .. (1979)
US-09-145-391-1

Alignment Scores:

Pred. No.: 2.56e-85
Score: 955.00
Percent Similarity: 86.94%
Best Local Similarity: 85.14%
Query Match: 87.94%
DB: 3
Gaps: 2

US-09-809-545A-2 (1-203) x US-09-145-391-1 (1-2372)

QY 1 MetThrAenLYeAlaValaAnProTYrThraNGLYTIpLYsLeuAnProValVal 20
DB 1572 ATGACAAATTAATAAGACCGCTCAACCTTATATACAAATGCGTGAATAATCAGTTGG 1631

QY 21 GLVALAValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsnGln 40
 |||
 DB 1632 GGTGCACTTCACTCAAGTCCCGAATCTATGACGACGCTCTGTTGTCACGACCAACAG 1691
 QY 41 GlnGlySerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
 |||
 DB 1692 GAAGGATCTTCATGTAAGAGTGGCCCGAGTTCACTGTATATCTTCTGCAATGCCAGGC 1751
 QY 61 PheProTyrProAlaAlaThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 80
 |||
 DB 1752 TTCCTGATCCAGAGCCAGCCGCGCGCCCTACGAGGCGGACCTGCGAGGCGC 1811
 QY 81 GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProProPheProAlaTyr 100
 |||
 DB 1812 GGTGCACTGTAACACACTTCAAGGCGCGCGCCCGCCCGCCCGGATCCGCGCTAC 1871
 QY 101 GlyValValValTyr-GlnGluProValTyrGlyAsnLysLeuGlnGlyTyrAla 120
 |||
 DB 1872 GGGGTGTGTGTTATCCAGATGATTTATGTCAGAC--ATTATGTTGTTATGC 1928
 QY 120 AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaAlaTyrSerAspSer 138
 |||
 DB 1929 TGCATACCGCTACCGCCAGCCTACCCCTGCACTGCGCTACAGTACAG-AAATC 1987
 QY 139 -----TyrGlyArgVa 142
 |||
 DB 1988 AGTTCGCTTCTGTCACGACGATGAATTTCTTGAACACTCTGCACTTACGACAGT 2047
 QY 142 TTYAAlaAlaAspProTyrHisIsthLeuAlaProAlaProThrTyrGlyValGlyAla 162
 |||
 DB 2048 TTATGCTGCGGACCCCTACGACGACGACCTTGTCCAGCCCGCCACTACGCGCTGTGTC 2107
 QY 162 aMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAspValGly 182
 |||
 DB 2108 CATGAAGCTTTGTCACCTTGTACTGATGCCAAGCTAGAGGATCTGATGATGAGGG 2167
 QY 182 YLeuValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyTyrAsnArgPheAlaPro 202
 |||
 DB 2168 TCTGCTTCTTCTTCAITTCAGGCTAGTATATACGAGGGGATACACCTTTGCTCC 2227
 QY 202 QTYr 203
 |||
 DB 2228 ATAC 2231

RESULT 2
 US-09-176-657-5
 ; Sequence 5, Application US/09176657
 ; Patent No. 6020164
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Lu, Aina
 ; APPLICANT: Baughn, Mariah R.
 ; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
 ; FILE REFERENCE: PR-0611 US
 ; CURRENT APPLICATION NUMBER: US/09/176,657
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 5
 ; LENGTH: 1506
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: 1250374
 US-09-176-657-5
 Alignment Scores:
 Pred. No.: 2,84e-37 Length: 1506
 Score: 467.50 Matches: 107

Percent Similarity: 56.48% Conservative: 15
 Best Local Similarity: 49.54% Mismatches: 39
 Query Match: 43.05% Indels: 56
 DB: 3 Gaps: 8

US-09-809-545a-2 (1-203) x US-09-176-657-5 (1-1506)

QY 1 MetThrAsnLysValValAlaAsnProTyrThrAsnGlyTyrLysLeuAsnProValVal 20
 |||
 DB 768 ATGACCAATAGAAAGATGGTCAACCATATGCAAAATGTTGAAATTAAGCCAGTAGTT 827
 QY 21 GlyValValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsn 39
 |||
 DB 828 GAGCTGTATATGCTCCGAGGTATATGACGATCCACGCTTCAACAGATGTCTCTTA 887
 QY 40 ---GlnGlnLysSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
 |||
 DB 888 GGCATATGATGACACAGTCCCTATACGAAAGGGGGATACACTTATCTCTTA 947
 QY 57 AlaMetProGlyPheProTyrPro--AlaAlaThrAlaAlaAlaAlaTyrArgGlyAla 75
 |||
 DB 948 ATGATTCCTGCTTCTTCTTACCTACTGAGCCAGCAGCAGCCGCTTCAAGAGAGCC 1007
 QY 76 HisLeuArgGlyValArgLysThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95
 |||
 DB 1008 CATTTGAGGGGACAGAGGGGAGACGATATGTCAGATCCGA---GGGTACCTCCAA 1064
 QY 96 ProIleProAlaTyrGlyValValTyrGlnLysProValTyrGlyAsnLysLeu 115
 |||
 DB 1065 GCCATCCCGCTTATC----- 1081
 QY 116 GlnGlyValTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
 |||
 DB 1082 AGGGGTGATATGACGCTTACATATGCAACCTGCTACTGCAACCGCAGCCAGCCGT 1141
 QY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
 |||
 DB 1142 GCTGACCGCTGACGCGCTTACAGTGAAGTTATGCGAGGGGTATACAGCGGACCCC 1201
 QY 148 TyrHisIsthLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
 |||
 DB 1202 TAC--CATGCCCTTCCCTCCCTGCGCTAGCTATGAGATTGCGCTGTG----- 1246
 QY 168 ProLeuThrAspAlaLysThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
 |||
 DB 1246 ----- 1246
 QY 188 LeuGlnAlaSerIleTyrGlnGlyTyrAsnArgPheAlaProTyr 203
 |||
 DB 1247 -----GCCAGTTTATACCGAGGTGCTACAGCCGATTGCCCCCTAC 1288
 RESULT 3
 US-09-421-299-5
 ; Sequence 5, Application US/09421299
 ; Patent No. 6524579
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Lu, Aina
 ; APPLICANT: Baughn, Mariah R.
 ; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
 ; FILE REFERENCE: PR-0611 US
 ; CURRENT APPLICATION NUMBER: US/09/421,299
 ; CURRENT FILING DATE: 1999-10-20
 ; EARLIER APPLICATION NUMBER: 09/176,657
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 5
 ; LENGTH: 1506
 ; TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 1250374
US-09-421-299-5

Alignment Scores:

Pred. No.:	2,84e-37	Length:	1506
Score:	467.50	Matches:	107
Percent Similarity:	56.48%	Conservative:	15
Best Local Similarity:	49.54%	Mismatches:	39
Query Match:	43.05%	Indels:	56
DB:	4	Gaps:	8

US-09-809-545a-2 (1-203) x US-09-421-299-5 (1-1506)

```

Qy 1 MetThrAsnLysValAlaAsnProDyThrsnGlyTrpLysLeuAsnProVal 20
    |||
Db 768 ATGACCAATAGAGATGTCACACCAATGCAATGAGAAATTAAACCCAGTAGTT 827
    |||

Qy 21 G1ValAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsn 39
    |||
Db 828 GGAAGCTTATATGTCCTCGAGATTATATGCAAGCATTCAGCATGAGATGTCCTTA 887
    |||

Qy 40 ---GlnGlyLysSerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
    |||
Db 888 GGCATGATGACAGAGTGCCTCTACAGAAAGGGGGTATCAACACTTACATTCCTTTA 947
    |||

Qy 57 AlamefProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaAlaTyrAlaGlyAla 75
    |||
Db 948 ATCATCTTCGCTGCTTCCCTTACCTTACCTGACAGCCAGCGAGCGCTTTCAGAGAGGCC 1007
    |||

Qy 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95
    |||
Db 1008 CATTGAGGGGAGAGGGGCGGACGATATGTCGACATCCGA---GGCGTACCTCCACACA 1064
    |||

Qy 96 ProIleProAlaTyrGlyGlyValValValTyrGlnGluProValTyrGlyAsnLysLeu 115
    |||
Db 1065 GCCATCCCGCCCTATCC----- 1081
    |||

Qy 116 GlnGlyGlyTyrAlaAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
    |||
Db 1082 AGGGGTGATATGAGCGCTACAGATATGCAAGCGTCTCTACTGACCCGAGCCAGCCGCT 1141
    |||

Qy 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
    |||
Db 1142 GCTGCAGCCGCTGACGCCGCTTACAGTACGCGTTATGCGAGGTGTACACAGCCGACCC 1201
    |||

Qy 148 TyrHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
    |||
Db 1202 TAC---CATGCCCTTGGCCCGCCGCTAGCTAGAGTTGGCGCTGG----- 1246
    |||

Qy 168 ProLeuThrAspAlaLysThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
    |||
Db 1246 ----- 1246
    |||

Qy 188 LeuGlnAlaSerIleTyrGlnGlyTyrAsnArgPheAlaProTyr 203
    |||
Db 1247 -----GCGAGTTTATCCAGAGGTGCTACAGCCGATTTGCCCTTAC 1288
    |||

```

RESULT 4

US-08-935-450-10
Sequence 10, Application US/08935450
Patent No. 597311
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Yang, Melija
APPLICANT: Schulz, Vincent
TITLE OF INVENTION: 53BP2 COMPLEXES
FILE REFERENCE: 7934-054
CURRENT APPLICATION NUMBER: US/08/935,450
CURRENT FILING DATE: 1997-09-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10
LENGTH: 914
TYPE: DNA
ORGANISM: Homo sapiens
US-08-935-450-10

Alignment Scores:

Pred. No.:	0.303	Length:	914
Score:	101.00	Matches:	48
Percent Similarity:	37.06%	Conservative:	15
Best Local Similarity:	28.24%	Mismatches:	59
Query Match:	9.30%	Indels:	48
DB:	2	Gaps:	7

US-09-809-545a-2 (1-203) x US-08-935-450-10 (1-914)

```

Qy 24 TyrSerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsnGlnGlySer 43
    |||
Db 230 TACAGCCCT-----GCTCGAAACCCCGAGGGGCC 259
    |||

Qy 44 SerMetTyrSerGlyProSerSerLeuValTyrThrSerAla-MetProGlyPheProTyr 63
    |||
Db 260 AGCAGCTACAAATAGAGACAGCAATCCCTGCTCAGGCGCAATACAGACACCCACCC 319
    |||

Qy 63 rProAlaAlaThrAla-----AlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 81
    |||
Db 320 GTCAGCAGCTACAGCCCTTCCACAGCCGAGTTACAGCCAGCCACTAC---AACAGGG 376
    |||

Qy 81 yArgThrValTyrAsnThrPheArgAlaAlaAla-ProProProProlleProAlaTyrG 101
    |||
Db 377 GAGGTACAGCAGGAGGTACAGAGGCCACCGCTCCACCTCCACACACACCTGCTTACA 436
    |||

Qy 101 yGlyValValTyrGlnGluProValTyrGlyAsnLysLeuGlnGlyTyrAla 121
    |||
Db 437 AC-----TATGGAGC-----TACGGCGGTACACCC 463
    |||

Qy 121 laTyrArgTyrAlaGlnProThrProAlaThrAlaAlaTyrSerAspSerTyrGlyAla 141
    |||
Db 464 CGGCCCTTATACCCAGCCGACCCCGCCAGCCAGACGCTTAC----- 507
    |||

Qy 141 rGValTyrAlaAlaAspProTyrHisThrLeuAlaProAlaProThrTyrGlyValG 161
    |||
Db 508 -----CCTCAGCCCACTTATACCACT 529
    |||

Qy 161 yAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAspAsp 181
    |||
Db 530 ATCAGCAGTATGCGAGCAGTGAACCACTATCTAGAACCAAGGCCAGT----- 579
    |||

Qy 181 aGlyLeuValLeuSerSerLeuGln 189
    |||
Db 580 ---GGCCCACTTACCGGAACCTACGA 603
    |||

```

RESULT 5

US-08-990-823-62
Sequence 62, Application US/08990823D
Patent No. 6228371
GENERAL INFORMATION:
APPLICANT: Nano, Francis
APPLICANT: Mycobacterium tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Immunostimulatory Peptides
FILE REFERENCE: 49086
CURRENT APPLICATION NUMBER: US/08/990,823D
EARLIER APPLICATION NUMBER: US 96/10375
EARLIER FILING DATE: 1997-12-15
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: 60/000,254
EARLIER FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 62
LENGTH: 821
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis

```

; FEATURE:
; NAME/KEY: Modified base
; OTHER INFORMATION: n represents a or g or c or t/u
US-08-990-823-62

```

Alignment Scores:

Pred. No.:	0.464	length:	821
Score:	98.50	Matches:	59
Percent Similarity:	28.46%	Conservative:	15
Best Local Similarity:	22.69%	Mismatches:	95
Query Match:	9.07%	Indels:	91
DB:	3	Gaps:	9

US-09-809-545A-2 (1-203) X US-08-990-823-62 (1-821)

Oy MeThrsAnlyslValAlaAenPrOlyrThrsAnGlyTrpLyLeuAsnProValVal 20
 Db 70 ATGGCCGACGACGTGCTGGCCGAGCCGAGCCCAATGCCGAGCATCTGCACCGGTTCCG 125
 Oy 21 G1yAlaValTySerProAapPhetyrAlaGlyThrValLeuLeuCyGAlaAlaAsnGln 40
 Db 130 GGGCAGCGCTTCGAGCCGAGCGGACGCTGGCGGATCATGCTCCGTCGGCTTCAAAACCGG 185
 Oy 41 GluGlySerSerMetTySerGlyProSer-----SerLeuValTy 54
 Db 190 AGGCGCGTGGCGGAGCACTCAATCTGCAGACCCGATGCTCCAAACCCGAGCTGATCAAC 245
 Oy 55 ThrSerAlaMetProGlyPheProTyProAlaAlaThrAlaAlaAlaAlaTyArgGly 74
 Db 250 TCGATGCTGTCGCCCAACAACCAAGCCGCATCATCCGACTCCGCGGGACGCGCGGA 305
 Oy 74 ----- 74
 Db 310 GGGAAAGGCCCCGGATCCGGATTCNCAAGGGTGGCNAAGCGGCGCTGCTGGATTTGGA 365
 Oy 75 -----AlaHisLeuAlaGlyArg-----GlyArgThrValTy 85
 Db 370 CCGCGCACATACCCCGGTATGGGACGTACGGGGAGAACACCTGGGCGGACGGCCAC 425
 Oy 86 AsnThrPheArgAlaAlaAlaProProProPoiLeProAlaTyGlyGlyValValTy 105
 Db 430 CTGGGCTGTACCAAGTTACCGGCCCGGACCCGAGCCGGCGGTGGT----- 485
 Oy 106 GlnGluProValTyGlyAlaValys-----LeuLeuGlnGly 115
 Db 481 -----GGTTTCGGCGCGCGCCCATCTGCTCTTACAAGAGAGAGACGGCGATTCATCTA 534
 Oy 119 -----TyralaAlaTyArgTyAlaGlnProThrProAlaThr 133
 Db 535 CGGCCAGTCCCTGAACCTGCAGTGGGGCGCTCACCGGCGCGGCGCATTCACCACT 594
 Oy 132 AlaAlaAlaTySerAspSerTy----- 135
 Db 595 GGGGACGATTTTCATGCATCACTGGAGACCGCAACCCGGGTGGCCATTCGGGTTCC 655
 Oy 140 -----GlyArgValTyAlaAlaAspProTyHis----- 155
 Db 655 GCTGGCTGGGCGCGCGGAGGCGCAAGTGGGCG-----CATGTCGC 695
 Oy 151 -----ThrLeuAlaProAlaProThrTyGly 155
 Db 700 CTATGACCCGAACTGAGCCCTGAGCAATGTTCCGCTTACACCCGCGGGTTCCGCT 755
 Oy 160 ValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaAlaTyThrsSerHisAlaAsp 175
 Db 760 GCTGGATCTCTGACGCGGTGATTCGGGTACAGGACACCGGTTGATGAGACATCGCAC 815

RESULT 6
 US-09-477-135A-62
 ; Sequence 62, Application US/09477135A
 ; Patent No. 6572865
 ; GENERAL INFORMATION:
 ; APPLICANT: Nano, Francis

TITLE OF INVENTION: Mycobacterium tuberculosis DNA Sequences Encoding
 TITLE OF INVENTION: Immunosimulatory Peptides
 FILE REFERENCE: 5288
 CURRENT APPLICATION NUMBER: US/09/477,135A
 CURRENT FILING DATE: 2000-01-03
 PRIOR APPLICATION NUMBER: 08990823
 PRIOR FILING DATE: 1997-12-15
 PRIOR APPLICATION NUMBER: US 96/10375
 PRIOR FILING DATE: 1996-06-14
 PRIOR APPLICATION NUMBER: 60/000,254
 PRIOR FILING DATE: 1995-06-15
 NUMBER OF SEQ ID NOS: 169
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 62
 LENGTH: 821
 TYPE: DNA
 ORGANISM: Mycobacterium tuberculosis
 FEATURE:
 NAME/KEY: variation
 LOCATION: (1)..(821)
 OTHER INFORMATION: n = A, C, G, or T
 US-09-477-135A-62

Alignment Scores:

Pred. No.:	0.464	821
Score:	98.50	59
Percent Similarity:	28.46%	Conservative: 15
Best local Similarity:	22.69%	Mismatches: 95
Query Match:	9.07%	Indels: 91
DB:	4	Gaps: 9

US-09-809-545A-2 (1-203) x US-09-477-135A-62 (1-821)

Oy	I	MetThrAsnLysbAlaValAsnProTyrThraEngLytrPblybLeuAsnProVal	20
Db	70	ATGGCCGACGACGTGCTGGCCGACCCCAATCCGGCGATGTGCAACCGGTCCG	123
Oy	21	GLYAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCyGlnAlaAsnGln	40
Db	130	GCGCAGCGCGTTGCGACCGGACCGAGCGCTGGGGCGGTATCAGTCCGGTGGCTTCAAAACCG	189
Oy	41	GlnGlySerMetTyrSerGlyProSer-----SerLeuValTyr	54
Db	190	AGGCGCTGGCGCGAGCACTCAAGTCCGAGNCCCGGATGTCCTCAAAACCGGCGTGTGCAC	249
Oy	55	ThSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyrArgGly	74
Db	250	TTCGATGCGTGGCCCAACAAACCAACGCGCATCATCGACTCGCGGACCGCCGCA	309
Oy	74	-----	74
Db	310	GGAAGGCGCCGAGTCCGGATTCACAGGGTTGCNACGGCGGCGTCCGCTTGNAGATTGGA	368
Oy	75	-----AlaHisLeuArgGlyArg-----GlyArgThrValTyr	85
Db	370	CCCGGACAGTACCCCGGTGATGGAGAGCTACCGGAGAAACCTGGCGCGCACCGGCAC	428
Oy	86	AsnThrPheArgAlaAlaAlaProProProProlIleProAlaTyrGlyGlyValValTyr	105
Db	430	CTCGGCGCTGTACCACTTACCGCCCGCGACCGCGGACCGGCGCGTGGGT-----	488
Oy	106	GlnGluProValTyrGlyAsnLys-----LeuLeuGlnGlyGly-----	118
Db	481	-----GGTTCCGCGCGCGCGGCATCTGGTCTCTACAGAGGAGCGCGCATTCATCTA	534
Oy	119	-----TyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr	133
Db	535	CGGCGACGTCCTGAACCTGACAGTGGGGGCTCACCGCGCCGAGCGCGCATTCAGCACT	594
Oy	132	AlaAlaAlaTyrSerAspSerTyr-----	138
Db	595	GAGGCGAGTATTTCCATGCATGCAGACCGACCGACCCGCTGGCGCAATCTGCGGTTCC	654

QY 140 -----GlyArgValTyrAlaIleAspProTyrHis----- 150
DB 655 GCTGCGTGGCGCCGCGGAGCGCGCGTGGCGC-----CATTTGCGC 699
QY 151 -----ThreAlaProAlaProThrTyrGly 159
DB 700 CTATGACCCCAACCTGAGCCCTGAGCAATGTTGCTTCAACCCCGCGGTTCGGT 759
QY 160 ValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAsp 179
DB 760 GCTGGAACTCTCTGACGCGGTGATTGCGGTGACGACACCGGTGTGATGACATCGCGAC 819

RESULT 7
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 6.01e+04 Length: 4403765
Score: 97.50 Matches: 66
Percent Similarity: 30.91% Conservative: 19
Best Local Similarity: 24.00% Mismatches: 95
Query Match: 8.98% Indels: 96
DB: 3 Gaps: 12

US-09-809-545A-2 (1-203) x US-09-103-840A-2 (1-4403765)

QY 1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTyrLysLeuAsnProValAl 20
DB 4237678 ATGGCCGACGACGTGCTGGCCGACGCCGACCAATGCCGGCATGCTGCAACCGGTTCCG 4237737
QY 21 GlyAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAlaAsnGln 40
DB 4237738 GGCACGCGCTTGGACCGGACGCGCGGTGATGATGCTCCGCGGCTTCAAAACC 4237797
QY 41 Glu-----GlySerSerMetTyrSerGlyPro-----SerSerLeuValTyr 54
DB 4237798 GAGGCGGTGGGCGACGACCTCAAGTCCGACCCGCTGCTCCAAACCCGGCGGTGTCAC 4237857
QY 55 ThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyrArgGly 74
DB 4237858 TCCGATGCTGCTGCGCCCAACCAACCGCGCATCAGCATCCGCGGCGACCGCGGCA 4237917
QY 75 AlaHisLeuArgGlyArgGlyArgTyrValTyrAsnThrPheArgAlaAlaAlaPro-- 93
DB 4237918 -----GGAAAGGCGCGGTGGGATCAACGGGTGCGACGGGCGGTGCGGTTCC 4237965
QY 94 -----ProProPheProAlaTyrGly----- 101
DB 4237966 GGAATTGACCCGCGACGTACCCGCGGTGATGGGACGTAACGGGAGAGAAACAACCTGGCGGCC 4238025
QY 102 -----GlyValValTyrGlnGluPro----- 108

DB 4238026 ACGGCCACCTCGGCGCTGTGATCAGATTACCGCCCGACGCCGAGCCGCGTGTGCTG 4238085
QY 109 -----ValTyrGlnAla 112
DB 4238086 GTTTCGCGCGCGCGCCCATCTGCTGCTTCAAGAGAGACCGGATTTCACTACGGCCAG 4238145
QY 113 LysLeu---LeuGlnGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
DB 4238146 TCCCTGAATCTGCAAGTGG-GGG-----GGTCAACCGCGCGGACCGCGCATCCAGCACT 4238198
QY 132 AlaAlaAlaTyrSerAspSerTyr----- 139
DB 4238199 GGGGCGAGTATTTCGATGACATCGACCGCAACCCGCGTGGCGCAATCTGCGGTTTCC 4238258
QY 140 -----GlyArgValTyrAlaAlaAspProTyrHis----- 150
DB 4238259 GCTGCGCTGGCGCGCGCGGAGCGCGACGTGGCGC-----CATTTGCGC 4238303
QY 151 -----ThreAlaProAlaProThrTyrGly 159
DB 4238304 CTATGACCCCAACCTGAGCCCTGAGCAATGTTGCTTCAACCCCGCGGTTCGGT 4238363
QY 160 ValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaLysThrArgSerHisAlaAsp 179
DB 4238364 GCTGGAACTCTCTGACGCGGTGATTGCGGTGACGACACCGGTGTGATGACATCGCGAC 4238423
QY 180 AspValGlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGln 194
DB 4238424 CCGACGCAACTT-----CCCTGCGAGCGACCGTTTCCGA 4238459

RESULT 8
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 6.02e+04 Length: 4411529
Score: 97.50 Matches: 66
Percent Similarity: 30.91% Conservative: 19
Best Local Similarity: 24.00% Mismatches: 95
Query Match: 8.98% Indels: 96
DB: 3 Gaps: 12

US-09-809-545A-2 (1-203) x US-09-103-840A-1 (1-4411529)

QY 1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTyrLysLeuAsnProValAl 20
DB 4245432 ATGGCCGACGACGTGCTGGCCGACGCCCAATGCCGGCATGCTGCAACCGGTTCCG 4245491
QY 21 GlyAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAlaAsnGln 40
DB 4245492 GGCACGCGCTTGGACCGGACGACCGCTGCGGTGATGATGCTCCGCTGCTTCAAAACC 4245551
QY 41 Glu-----GlySerSerMetTyrSerGlyPro-----SerSerLeuValTyr 54

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Db 424552 GAGGCGGTGGCGAGACCTCAAGTCGACCCGGGTGTCCTCAAAACCGGGCTGTCAAC 4245611
Qy 55 ThSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgGly 74
Db 4245612 TCCGATGCGCGCCCAACCAACCGCCGATCCGACCTCCGGCGGACCGCCGGA 4245671
Qy 75 AlaHleuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaPro--- 93
Db 4245672 -----GGGAAGGCGCGGTGGGATGACAGCGGTGCGACCGGGCGTCCGCTTC 4245719
Qy 94 -----ProProIleProAlaTyrGly----- 101
Db 4245720 GATTGGAACCGGACGACCGCGGTATGAGGAGCTACGGGAGAACCACTGGCGCC 4245779
Qy 102 -----GlyValValTyrGlnGluPro----- 108
Db 4245780 ACGGCCACTCGCGCTGTACAGTTACCGCCCGACCGGACCGCGCTGTGTG 4245839
Qy 109 -----ValTyrGlyAsn 112
Db 4245840 GTTTCGCGCGCGCGCATCTGTCTTACAGAGAGACGGCATTTTCATCTACGGCAG 4245899
Qy 113 LysLeu---LeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
Db 4245900 TCCCTGAACCTGAGTG-GGG-----CGTCACGCGCGCGGACGGCGCATCCAGCAGCT 4245952
Qy 132 AlaAlaAlaTyrSerAspSerTyr----- 139
Db 4245953 GGGGCGAGGTATTTCCGATTCAGCAACCGGACCGCGCATCTCGCGTTTC 4246012
Qy 140 -----GlyArgValTyrAlaAlaAspProTyrHisHis----- 150
Db 4246013 GCTGGCTGGGCGCGCGGAGCGGACGCGGCG-----CATTTGCG 4246057
Qy 151 -----ThrLeuAlaProAlaProThrTyrGly 159
Db 4246058 CTATGACCCGAACTGAGCCCTGAGCAATGGTTGCTTCCACCGCGCGGTTCCGCT 4246117
Qy 160 ValGlyAlaMetAlaAlaPheAlaProLeuThrAspAlaThrArgSerHisAlaAsp 179
Db 4246118 GCTGGAACTCTCTGCGAGGTTGATCGGATCGACACCGGTGTTGATGACATCGCGAC 4246177
Qy 180 AspValGlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGln 194
Db 4246178 CGCAGCCAACTT-----CCCTTCGACGACCGCTTTCCGA 4246213

RESULT 9
; Sequence 1, Application US/08195152
; Patent No. 5679541
; GENERAL INFORMATION:
; APPLICANT: Bonini, Nancy M.
; APPLICANT: Leiserson, William M.
; APPLICANT: Benzer, Seymour
; TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohenbach, Teet, Albritton & Herbert
; STREET: 4 Embardadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,152
; FILING DATE: 14-FEB-1994

```

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Treacartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; US-08-195-152-1

Alignment Scores:
Pred. No.: 5.2 Length: 3231
Score: 96.00 Matches: 45
Percent Similarity: 37.57% Conservative: 23
Best Local Similarity: 24.86% Mismatches: 63
Query Match: 8.84% Indels: 51
DB: 1 Gaps: 6

US-09-809-545a-2 (1-203) x US-08-195-152-1 (1-3231)

Qy 42 GlySerSerMetTyr-----SerGlyProSerSerLeu 52
Db 1062 GGAATCAATTGTGACGGCTGCGACCTGCGGACCAATCCGTGACGAGAGACAGTGGCG 1121
Qy 53 ValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyr 72
Db 1122 GTCACTCTTCGCGCAGT-----GACGCGGACGACGACGCGGTCTAC 1163
Qy 73 ArgGlyAlaHisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAla 92
Db 1164 GAGCGCAACAT-----GACTACTACTACTACAAACAGCATGACGACGTACAGC 1211
Qy 93 ProProIleProIleProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsn 112
Db 1212 CCGCGCGCTTCTTACCTCCGATACGAACTCTTATGCGCGGCAACGGCGGACGCGAG 1271
Qy 113 LysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThrAla 132
Db 1272 GCCAAGTGAACCGGAGGCGGAGCTGCGCGGCTGCTTACGCGCCAGCTAGGCC 1331
Qy 133 AlaAla----- 134
Db 1332 GCCAGCGCAACAACTGCGAGCTGTACAGAGTCCGTACCGCGGCTACAACTTC 1391
Qy 135 -----TyrSerAspSerTyrGlyArgValTyrAlaAlaAsp 146
Db 1392 GGGCAGCAGACTACGCGCGCTACTACAGACGACGACGACGACGACGACGACGACG 1451
Qy 147 ProTyrHisThrLeuAlaProAlaPro-----ThrTyrGlyValGly--- 161
Db 1452 AACTACACCGATGCGGTGCGAGCTGCGCGGACGCTGAGTGCAGTGCAGTGCAGTGC 1511
Qy 162 AlaMetAlaAlaPheAlaProLeuThrAspAlaThrArgSerHisAlaAspVal 181
Db 1512 CATGTGCGCGCTCTCGAATCTCTCGAAGATCCCGACGACCACTC-GACGAGCGCC 1570
Qy 182 Gly 182
Db 1571 GGT 1573

RESULT 10
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLBISCHMAN, Robert D.

```

```

; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 1.16e+05 Length: 4403765
Score: 94.50 Matches: 49
Percent Similarity: 42.26% Conservative: 22
Best Local Similarity: 29.17% Mismatches: 68
Query Match: 8.70% Indels: 31
DB: 3 Gaps: 8

US-09-809-545a-2 (1-203) x US-09-103-840A-2 (1-4403765)
QY 11 ThranglYTrpYsLeuAnProValValGlyAlaValYrSerProAspPheTYrAla 30
Db 991136 ACAATGAGAGCTGTGCAATCTCTACTGCGGGGGTGGAGACT--GCATATCAG 991080
QY 31 GlyThrValLeuLeuGyGlnAlaSnGlnGlySerSerMetTYrSerGlyProSer 50
Db 991079 GTGACCGCAATGCTTGTGAGCCGCGCAGAAAGATCCGCGACCTGGCCGACACCATCG 991020
QY 51 SerLeu-----ValTYrThrSerAlaMetProGlyPheProTYrProAlaAlaThrAla 68
Db 991019 GCGACCGGTTGCTGTCAGTCAGCTGAGCTTGTGCTTATTTGGCCGAGATGGGCTG 990960
QY 69 Ala-----AlaAlaTYr-ArgGlyAlaHisLeuArgGlyArgGly----- 81
Db 990959 GCATCTGACCGAGACCCCTGAGCTATCCAGGAAATCATCGCGAGGCGAGGCATCCA 990900
QY 82 -----ArgThrValTYr-----AsnThrPheArgAlaAl 91
Db 990899 ACGATGTGCGGACAAAGATTCTCGCCTATATACCCAAAGCCAGGTGC-TGGCGTATTGC 990841
QY 91 AlaProProProProProProProProProProProProProProProProProProProPro 111
Db 990840 GCGCCGACCGCGCGCGCGCCATA-GCGGGGCGCTGATTCAGCCCGCGAGGATTAGG 990782
QY 111 YAsnLYLeuLeuGlnGly---GlyTYrAlaAlaTYrArgTYrAlaGlnProProAl 130
Db 990781 CCGG---GTGACCAAGAGCATGTTATGCGGCATACGTAAGC----- 990739
QY 130 arhAlaAlaAlaTYrSerAspSerTYrGlyArgValTYrAlaAlaAspProTYrHisAl 150
Db 990738 ----GCGCTGGCGCGCGGTATGTACAGCGAGCGCTGAGGCGCAGCAGCGGGCGCGCG 990683
QY 150 sThrLeuAlaProAlaProThr 157
Db 990682 ATTCTTAGGGCCGCGCGAC 990661

RESULT 11
; Sequence 3, Application US/09343011B
; Patent No. 6306473
; GENERAL INFORMATION:
; APPLICANT: Stephanie Richard
; TITLE OF INVENTION: SLM-1 AND SLM-2; NOVEL
```

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; TITLE OF INVENTION: SAM68-LIKE MAMMALIAN PROTEINS
; FILE REFERENCE: A32561
; CURRENT APPLICATION NUMBER: US/09/343.011B
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: CA 2265271
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2368
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-343-011B-3

Alignment Scores:
Pred. No.: 5.4 Length: 2368
Score: 94.00 Matches: 54
Percent Similarity: 36.93% Conservative: 11
Best Local Similarity: 30.68% Mismatches: 51
Query Match: 8.66% Indels: 60
DB: 4 Gaps: 12

US-09-809-545a-2 (1-203) x US-09-343-011B-3 (1-2368)
QY 73 ArgGlyAlaHisLeuArgGlyArgGlyArgThrValTYrAsnThrPhe----- 88
Db 1673 CGGGCGGAGCTATTAGGACAGAGGATCAGATATACCTCCACAGCTCATCAGAGGCG 1732
QY 89 ArgAlaAlaAlaProProProProProProProProProProProProProProProPro 108
Db 1733 CGTGGCGGTGCTTGTCCACACACACACACACCTGAGAGAGTGTCTTACCCCTCG-- 1789
QY 109 ValTYrGlyAsnLYLeuLeuGlnGly----- 117
Db 1790 -----GGACCACTGTGACCCCTGAGCTTTCAGTGCCTCCCATAGCAAGAGTGC 1843
QY 118 -----GlyTYrAlaAla-----TYrArgTYrAlaGlnProThr 128
Db 1844 CCACACCTGAGACCGCGGGGAGCGGAGAGTACAGATACAGA--GCACCCCACT 1900
QY 129 ProAlaThrAlaAla-----AlaTYrSerAspSerTYrGlyArgValTYrAla 144
Db 1901 CCAGCTCATGATCTTATGAAAGATATGCTATGATGATGCTATGGGTGGAATGAT 1960
QY 145 AlaAspProTYr-----HisHisThrLeuAlaProAlaProThr----- 157
Db 1961 GACCAAGACCTATAGGCTTATGATATAGCTACGTGACCCCAACACAAAGTGCCTGAA 2020
QY 158 -----TYrGlyValGly-----AlaMetAsnAlaPheAlaProLeuThr 170
Db 2021 TACTATGACTACGCTGATGAGTAAGAGAGATGCTTACAGACGTAAGCAGCAAGAA 2080
QY 171 AspAlaLYSerThrArgSerHisAlaAspAspValGlyLeuValLeuSerSerLeuGlnAla 190
Db 2081 TGGGCAACAACCTGC-----TCCAGCTGAAAGGCA 2110
QY 191 -----SerLeTYrGlnGlnGlyTYrAsnArgPheAlaProTYr 203
Db 2111 CCACCAACAAGTACAGCAGAGGGGATAC--AGGAGACACCCCTAT 2155

RESULT 12
US-08-804-227C-1/C
; Sequence 1, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: Dehoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Roestek, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
```

[illegible]

```

Qy 91 LaAlaProProProProProLeProAlaTyGlyGlyValValTyGlnGProValTyr 110
Db 7951 GCCATGCTCTCCCCCGCCCAAGAGCCCCCAGCGCAGAGAGTTCGCGGCGCATGCCGCGCA 7892
Qy 111 GlyAsnLysLeuLeuGlnGlyGlyTyraAlaAlaTyraGlyTyrAla--GlnProThrPro 129
Db 7891 CGCGGACGGCTCGGCGCGGCGCTCGAGCGCGCGGCTTGCGCGCGCGCTACGACCCCTGCGCG 7832
Qy 130 AlaThrAlaAlaAlaTyrsersapserTyrGlyArgValTyraAlaAlaAspProThrs 149
Db 7831 GCGTTCGCCCATGTCGCCGTGACGAGAGGAAAGACGACGAGCGCTCCAACTCTTT--- 7775
Qy 150 HisThrLeuAlaProAlaProThrTyrglyValGlyAlaMetAsnAlaPheAlaProLeu 169
Db 7774 -----ATGTCGGCAGTCACTGATGGTGTCGACGACTCCGCGCCGACACCTTCGCGCGG 7721
Qy 170 ThrAspAlaLysThrArgserHisAlaAspAspValGlyLeuValLeuserserLeuGln 189
Db 7720 ACCGTCCTCGAAGCTC-----TCCGGTGCACACGCTGTCGATCACCAGCGCTCCAGAAATC 7667
Qy 190 AlaSerLetyrGln-----GlyGlyTyr 197
Db 7666 CCGCGCGTGTGGAAAGCGCGCTTCGCGGATAC 7634

RESULT 13
Sequence 1, Application US/08343443B
Patent No. 5968734
GENERAL INFORMATION:
APPLICANT: Aurias, Alain
APPLICANT: Delattre, Olivier
APPLICANT: Desmazes, Chantal
APPLICANT: Melot, Thomas
APPLICANT: Peter, Martine
APPLICANT: Ploougasdel, Beatrice
APPLICANT: Thomas, Gilles
APPLICANT: Zucman, Jessica
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLOCATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
TITLE OF INVENTION: TRANSLOCATIONS
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard U.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989, 6121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394

```

```

1      INFORMATION FOR SEQ ID NO: 1:
2      SEQUENCE CHARACTERISTICS:
3          LENGTH: 2371 base pairs
4          TYPE: nucleic acid
5          STRANDEDNESS: double
6          TOPOLOGY: linear
7      FEATURE:
8          NAME/KEY: CDS
9          LOCATION: 25..1992
10     US-08-343-443B-1
11
12     Alignment Scores:
13     Pred. No.: 7.61 Length: 2371
14     Score: 92.50 Matches: 48
15     Percent Similarity: 33.72% Conservative: 10
16     Best Local Similarity: 27.91% Mismatches: 73
17     Query Match: 8.52% Indels: 41
18     DB: 2 Gaps: 9
19
20     US-09-809-545A-2 (1-203) x US-08-343-443B-1 (1-2371)
21
22     QY 29 T Y R A I a g l y T h r V a l l e u e n C y s g i n a l a - - - A s n g i n g l u g l y S e r S e m e t Y s e r 47
23         ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
24     Db 109 T A T G C A C A G C C A C C - - - - - C A G C A T T A T G G G C A A C A A G C T A T G A A C C C A T G A 159
25
26     QY 48 G l y P r o S e r S e r l e u V a l l y T h r S e r a l A m e t P r o g l y P h e P r o t y P r o A l a T h r 67
27         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
28     Db 160 C A G C C C A C T A T G C A C T A T A C C A G G C C T C A G A C C A C C A C T G C A A C C T A T G G G C A G A C G C C 219
29
30     QY 68 A l a l a l a l a l a l y r a g l y a l a h i s l e u a r g l y a r g l y a r g T h r V a l l y T r a s n T h r 87
31         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
32     Db 220 T A T G C A A C T T C T T A T - - - - - G A C A G C C T C C A C G T G T T A T A C T A C T 261
33
34     QY 88 P h e a r g l a l a l a l a p r o p r o p r o l l e p r o a l a t y r g l y g l y v a l v a l l y r g i n g l u 107
35         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
36     Db 262 - - - - - C C A A C T G C C C C C A G - - - - - G C A T A C A G C C A G 288
37
38     QY 108 P r o v a l y T r g l y a n l y s l e u l e u g i n g l y g l y T r y a l a l a t y r a r g T r y a l g l n p r o 127
39         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
40     Db 289 C C T G C C A G G G G T A T - - - - - G G C A C T G G T G C T T A T A T A C C A C A C A C T G C T 333
41
42     QY 128 T h r P r o a l a h r a l a l a l a l a t y r s e r a s p s e r t y r g l y a r g v a l T r y a l a l a s p p r o 147
43         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
44     Db 334 A C A G T C A C C A C C A C C A G G C C - - - - - T C C T A T G C A G C T C A G T C T 372
45
46     QY 148 T y r h i s t h r l e u a l a p r o a l a p r o t h r T y r g l y v a l g l y a l a m e t a s n a l a p h e a l a 167
47         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
48     Db 373 G C A T A T G G C A C T A G C C T G T T A T C A G C C T A T G G C A G - - - - - C A G 414
49
50     QY 168 P r o l e u t h r a s p a l a y s t h r a r g s e r h i s a l a a s p a s p v a l g l y l e u v a l l e u s e r 187
51         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52     Db 415 C C A G C A G C A C T G C A C C T A C A A G C G A G A T G A A C A A C C A C C A C T A G A C T A G T C A A 474
53
54     QY 188 l e u g l a l a s e r l e t y r g i n g l y g l y T r y a n a r g 199
55         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
56     Db 475 C C T C A A T C T A G C - - - - - A C A G G G G T T A C A A C C A G 504
57
58     RESULT 14
59     US-08-437-027-18
60     Sequence 18, Application US/08437027
61     Patent No. 5670317
62     GENERAL INFORMATION:
63     APPLICANT: Landany1, Marc
64     APPLICANT: Gerald, William
65     TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
66     NUMBER OF SEQUENCES: 21
67     CORRESPONDENCE ADDRESS:
68     ADDRESSEE: Cooper & Dunham LLP
69     STREET: 1185 Avenue of the Americas
70     CITY: New York
71     STATE: New York
72     COUNTRY: U.S.A.

```

```

: ZIP: 00036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/437,027
: FILING DATE:
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 46616/JPM/CCA
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-278-0400
: TELEFAX: 212-391-0525
: INFORMATION FOR SEO ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2412 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: US-08-437-027-18

Alignment Scores:
Pred. No.: 7.79 Length: 2412
Score: 92.50 Matches: 48
Percent Similarity: 33.72% Conservative: 10
Best Local Similarity: 27.91% Mismatches: 73
Query Match: 8.52% Indels: 41
DB: 1 Gaps: 9

US-09-809-545A-2 (1-203) x US-08-437-027-18 (1-2412)

Oy 29 TTTAAGTGTThrValLeuLeuGluGlnA---AaGlnGlnGlnGlySerSerMetTyrSer 47
Db 109 TATGTCACAGCCACC-----CAGGCATATGGGCAACCAACTATGGAACCTATGGA 155
Oy 48 GlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThr 67
Db 160 CAGCCACCATGATGTCAAGCTATACCCAGGCTCAGACCACTGACAACTATGGCAGACGCC 219
Oy 68 AAlaAlaAlaTyrGlnGlyAlaHisLeuArgGlyArgGlyArgThrValTyrAsnThr 87
Db 220 TATGCAACTCTTAT-----GGACAGCCTCCCACTGGTTATTACT 261
Oy 88 PheaArgAlaAlaAlaProProProProIleProAlaTyrGlyGlyValValTyrGlnGlu 107
Db 262 -----CCAACTGCCCCCCAG-----GCATACAGCCAG 288
Oy 108 ProValTyrGlyAsnHisLeuLeuGlnGlnGlyTyrAlaAlaTyrArgTyrAlaGlnPro 127
Db 289 CCTGTCCAGGGGAT-----GGCATGTGTGCTTATGATACCAACCACTGCT 333
Oy 128 ThrProAlaThrAlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
Db 334 ACAGTCACACCAACCAACGAGCC-----TCCTATGACGCTCACTCT 372
Oy 148 TyrHisHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
Db 373 GCATATGCGCACTCAGCCTGCTTATCAGGCTATGGGCGAG-----CAG 414
Oy 168 ProLeuThrAspAlaAlaThrThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
Db 415 CCAGCAGCACTGCACTTACAAAGACCGACGATGAAACCAAGCCCACTGAGACTATGCAA 474
Oy 188 LeuGlnAlaSerTleTyrGlnGlnGlyGlyTyrAsnArg 199
Db 475 CCTCAATCTAGC-----ACAGGGGGGTTTAAACAGCA 504

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US-08-258-261B-6
Sequence 6, Application US/08258261B
Patent No. 5639949
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip B.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,261B
FILING DATE: 08-JUN-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-258-261B-6
Alignment Scores:
Pred. No.: 222 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 8.52% Indels: 12
DB: 1 Gaps: 4
US-09-809-545A-2 (1-203) x US-08-258-261B-6 (1-28958)
QY 47 SerGlyPProSerSerLeuValTyrThrSeraIawecProGlypheProTyrrProalaala 66
Db 10706 AGCGGCCTCTGGACAGATGGCATGTCTTCGCCGAGGCAAGCCACCCTCATCCGTCTCA 107655
QY 67 ThrAlaaalaaalaaTyr--ArgLylalahlis-LeuarGlylArgLyArGrThrValry 85
Db 10766 CGCTCGCCCTCGGAGAAGCTTGAGAGGCGTTACAAGCTCGATCCGTCGTCGAGCTCCA 108255
QY 85 rhanThearheargalaaalaaIapropoprioleprolatyrglyglyvalValry 105
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Db      10826 TTGGAGCG--AGAAAGAAAGGCACTCGCCGCGCTGCTCTCTCTGCGGAGACTCTCA 10882
Qy      105   rGInGluProValTyrGlyAseuLysLeuLeuInGlyGlyTyrAlaAlaTyrArgTyrAl 125
Db      10883 CCGGAGGCGCT-----CGCGCTCGATGGAGAGCACTCTTCGGCGCTTCAGCTCCCC 10933
Qy      125   aGIn-----ProThrProAlaThrAlaAlaTyrSerAspSerTy 139
Db      10934 GCAGAGCTTCCTCCCTCCCACTCACTCCCTTCAGGAGAGCGGTTCTGCTCGACGTCCTCA 10993
Qy      139   rGlyArgValTyrAlaAlaAspPro 147
Db      10994 CGAGCGAAGCCTTCGAGACTGCGCT 11018

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Search completed: January 15, 2004, 09:58:40
Job time : 3326.09 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2004, 08:51:30 ; Search time 191.852 Seconds

(without alignments)
2719.103 Million cell updates/sec

Title: US-09-809-545A-2_COPY_1_148

Perfect score: 796
Sequence: 1 MINKKAVNPYTNQMKLNPVY.....PATRAAYSDSYGRVADPY 148

Scoring table: BLOSUM62

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Fgapop 10.0	Fgapext 0.5
Delpop 6.0	Delext 7.0

Searched: 2324096 segs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-Q=/cg2_1/USPTO.spool_P/US09809545/runat_15012004_061052_2510/app_query.fasta_1.718
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsum62
-TRANS=human40.ctd -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

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12:	/cg2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:	/cg2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
14:	/cg2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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1	796	100.0	1340	10	US-09-809-545A-1	Sequence 1, Appl1
2	674	84.7	2372	9	US-09-794-591-1	Sequence 1, Appl1
3	441.5	55.5	1843	11	US-09-919-039-266	Sequence 266, App
4	430.5	54.1	1558	13	US-10-094-749-287	Sequence 287, App
5	379	47.6	1506	13	US-10-359-385-5	Sequence 5, Appl1
6	143	18.0	2397	12	US-10-104-047-659	Sequence 659, App
7	94	11.8	657	10	US-09-974-300-1855	Sequence 1855, App
8	92.5	11.6	699	13	US-10-027-632-24830	Sequence 24830, A
9	92.5	11.6	699	13	US-10-027-632-24831	Sequence 24831, A
10	92.5	11.6	699	13	US-10-027-632-24832	Sequence 24832, A
11	92.5	11.6	699	14	US-10-027-632-24830	Sequence 24830, A
12	92.5	11.6	699	14	US-10-027-632-24831	Sequence 24831, A
13	92.5	11.6	699	14	US-10-027-632-24832	Sequence 24832, A
14	92.5	11.6	11447	13	US-10-301-822-25	Sequence 25, Appl1
15	92.5	11.6	11447	15	US-10-177-293-60	Sequence 60, Appl1
16	92.5	11.6	11560	15	US-10-177-293-62	Sequence 62, Appl1
17	92.5	11.6	11567	15	US-10-198-846-11039	Sequence 11039, A
18	91	11.4	821	10	US-09-996-634-62	Sequence 62, Appl1
19	91	11.4	821	11	US-09-997-182-62	Sequence 62, Appl1
20	91	11.4	821	11	US-09-997-181-62	Sequence 62, Appl1
21	90	11.3	466	11	US-09-918-995-8298	Sequence 8298, App
22	89.5	11.2	1889	13	US-10-120-988-247	Sequence 247, App
23	89.5	11.2	3285	10	US-09-712-363-143	Sequence 143, App
24	89	11.2	1089	15	US-10-156-761-2855	Sequence 2855, App
25	89	11.2	9025608	15	US-10-156-761-1	Sequence 1, Appl1
26	87.5	11.0	2658	9	US-09-815-242-4035	Sequence 4035, App
27	87.5	11.0	3231	8	US-08-754-311B-1	Sequence 1, Appl1
28	87.5	11.0	10278	13	US-09-820-788-3	Sequence 20319, A
29	87.5	11.0	10278	13	US-10-094-749-1507	Sequence 1507, App
30	87	10.9	2200	13	US-10-369-493-45445	Sequence 45445, A
31	86.5	10.9	1587	12	US-10-205-219-182	Sequence 182, App
32	86	10.8	1963	13	US-10-027-632-97742	Sequence 97742, A
33	86	10.8	2179	13	US-10-027-632-97742	Sequence 97742, A
34	86	10.8	2179	14	US-10-369-493-31940	Sequence 31940, A
35	85.5	10.7	1960	12	US-10-094-749-1507	Sequence 1507, App
36	85.5	10.7	2208	13	US-10-027-632-97742	Sequence 97742, A
37	85.5	10.7	2208	15	US-10-037-270-502	Sequence 502, App
38	85	10.7	1055	13	US-10-029-386-20383	Sequence 20383, A
39	85	10.7	1383	15	US-10-156-761-3834	Sequence 3834, App
40	85	10.7	1743	10	US-09-887-846-1	Sequence 887, App
41	85	10.7	5352	14	US-10-094-749-1507	Sequence 1507, App
42	85	10.7	5352	11	US-09-904-968A-1	Sequence 904, App
43	85	10.7	9025608	15	US-10-156-761-1	Sequence 1, Appl1
44	84.5	10.6	969	13	US-10-244-830-452	Sequence 452, App
45	84.5	10.6	969	13	US-10-195-835-452	Sequence 452, App

ALIGNMENTS

RESULT 1
US-09-809-545A-1
Sequence 1, Application US/09809545A
Patent No. US2002010804A1
GENERAL INFORMATION:
APPLICANT: Stanton, Lawrence W.
TITLE OF INVENTION: SECRETED FACTORS
FILE REFERENCE: SCIOS 017A
CURRENT APPLICATION NUMBER: US/09/809,545A
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1340
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-809-545A-1

Alignment Scores:
Pred. No.: 6,97e-86 Length: 1340
Score: 796.00 Matches: 148
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-809-545a-2_copy_1_148 (1-148) x US-09-809-545a-1 (1-1340)

Qy 1 MetThrsAnlyblysaValaAsnProTyRThrsnGlyTPrlybLeuAsnProVala1 20
Db 535 ATGACATAATAAAGCCGCGTGAACCCCTACACCAATGGCTGGAATTAATCCAGTTGTG 594
Qy 21 G1yAlaVala1TyRserProAspPheTyRAlaGlyThrValleuCyGslna1aAsnGln 40
Db 595 GGGCCGGTCTACACCCCGGACTTCTATGACAGCGGCTGTTGTCCAGGCAACAG 654
Qy 41 GluGlySerSerMetTyRserGlyProSerSerLeuValTyRThrsAlaMetProGly 60
Db 655 GAGGAGCTTCCATGTCAGTGGCCCACTTCTGTAATTAATTCGCAATCCCTGGC 714
Qy 61 PheProTyRProAlaAlaThraAlaAlaAlaTyRArgGlyAlaHisLeuArgGlyArg 80
Db 715 TTTCATATCCGCGCCGACCTGTCAGCTGCATACGAGGGGCTCACCTTCGAGGCGCT 774
Qy 81 G1yArgThrValTyRAsnThrPheArgAlaAlaAlaProProProProlleProAlaTyR 100
Db 775 GGTGCAACCGTGTACCAACCTTCAGAGCTGGCGCCGCCCAATCCGCGCTAT 834
Qy 101 G1yGlyValaValaTyRglnGluProValTyRg1yAsnlybLeuGlnGlyGlyTyRAla 120
Db 835 GGGGAGTAGTGTATCAAGAGCCAGTGTATGCAATTAATGCTACAGGGGTATAGCT 894
Qy 121 AlaTyRArgTyRAlaGlnProThrProAlaThraAlaAlaTyRserAspSerTyRg1y 140
Db 895 GCATACCGCTACGGCCAGCCACCCCTGCTGCTGCTGCTACAGTACAGTACGGA 954
Qy 141 ArgVala1TyRAlaAspProTyR 148
Db 955 CGAGTTATGCTGCGACCCCTAC 978

RESULT 2

US-09-794-591-1
Sequence 1, Application US/09794591
Patent No. US20010018198A1
GENERAL INFORMATION:
APPLICANT: Pulet, Stefan M.
APPLICANT: Shibata, Hiroki
TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins.
FILE REFERENCE: CE 3093
CURRENT APPLICATION NUMBER: US/09/794,591
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/145,391
PRIOR FILING DATE: 1998-09-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (987) .. (1979)
US-09-794-591-1

Alignment Scores:
Pred. No.: 6,31e-71 Length: 2372
Score: 674.00 Matches: 136
Percent Similarity: 83.23% Conservative: 3
Best Local Similarity: 81.44% Mismatches: 8
Query Match: 84.67% Indels: 21
DB: 9 Gaps: 2

US-09-809-545a-2_copy_1_148 (1-148) x US-09-794-591-1 (1-2372)

Qy 1 MetThrsAnlyblysaValaAsnProTyRThrsnGlyTPrlybLeuAsnProVala1 20

Db 1572 ATGACAAAATAAAGACCGTCAACCTTATACAAATGGCTGGAATTAATCAAGTTGTG 1631
Qy 21 G1yAlaVala1TyRserProAspPheTyRAlaGlyThrValleuCyGslna1aAsnGln 40
Db 1632 GGTGCACTTACAGTGTCCCAATTTCTATGAGGACGCTCTGTGTGCCAGGCCAACAG 1691
Qy 41 GluGlySerSerMetTyRserGlyProSerSerLeuValTyRThrsAlaMetProGly 60
Db 1692 GAGGAGCTTCCATGTCAGTGGCCCACTTCTGTAATTAATTCGCAATGCGAGGC 1751
Qy 61 PheProTyRProAlaAlaThraAlaAlaAlaTyRArgGlyAlaHisLeuArgGlyArg 80
Db 1752 TTCCCTATCCACAGCACCCCGCGGCGCTTACCGAGGGGCGACCTGCAAGCGCGC 1811
Qy 81 G1yArgThrValTyRAsnThrPheArgAlaAlaAlaProProProProlleProAlaTyR 100
Db 1812 GGTGCAACCGTGTACCAACCTTCAAGGCGCGGCCGCCGCCGATCCGCGCTAC 1871
Qy 101 G1yGlyValaValaTyRglnGluProValTyRg1yAsnlybLeuGlnGlyGlyTyRAla 120
Db 1872 GGGGAGTTGTTTACCCAGATGATTTATGTCAGAC--ATTATGTTGTTATGC 1928
Qy 120 AlaTyRArgTyRAlaGlnProThrProAlaThraAlaAlaTyRserAspSer----- 138
Db 1929 TGCATACCGTACGCCACGACTACCCCTGCACTGCGCTTACAGTACAG-AAATC 1987
Qy 139 -----TyRg1yArgVa 142
Db 1988 AGTTCGCTTCTTTCGACGACGATGAATTTCTTGTACACCTGCAAGTTACGAGAGT 2047
Qy 142 1TyRAlaAlaAspProTyR 148
Db 2048 TTATGCTGCCGACCCCTAC 2066

RESULT 3

US-09-919-039-266
Sequence 266, Application US/09919039
Publication No. US2003010887A1
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 266
LENGTH: 1843
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US2003010887A1 253783.3
NAME/KEY: unsure
LOCATION: 1824
OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-266

Alignment Scores:
Pred. No.: 3,78e-43 Length: 1843
Score: 441.50 Matches: 96
Percent Similarity: 51.02% Conservative: 4
Best Local Similarity: 48.98% Mismatches: 19
Query Match: 55.46% Indels: 77
DB: 11 Gaps: 5

US-09-809-545a-2_copy_1_148 (1-148) x US-09-919-039-266 (1-1843)

Qy 1 MetThrsAnlyblysaValaAsnProTyRThrsnGlyTPrlybLeuAsnProVala1 20

Dbb

1228 ATGACCAACAAGAAAGACGGGAACCCCTACGCCAACCGCTGGAAGCTTAATTCAGTGGTC 1287

Qy 21 G1yAlaValIYrSerProAspPheTYrAlaGlyThrValLeuCySglnAlaSnGln 40
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Dbb 1288 GGCCACAGCTCAGCGGCCTGAAATTCTATGACGTGACG----- 1323

Qy 41 GluGlySerMetYTyrSerGlyProSerSerLeuValTYrThrSerAlaMetProGly 60
---|Gg 1326

Dbb 1324 ----- 1326

Qy 61 PheProTYrProAlaAlaThrAlaAlaAlaAlaTYrArgIYalAHisLeuArgGIYArG 80
|||

Dbb 1327 TTCCCCTRACCCACCACCGGACAGCGCTTGCTCACGGGGCGCAACATCTTCGGGGCCGG 1386

Qy 81 GIYArGThrValIYrAsnThr-PheArgAlaAlaAlaAlaProProProIlePreAlaTYr 100
|||

Dbb 1387 GGCGGGGGCGGTGTATAATACATTTCCGGCTCGCCACCCCACCCCCATCCGACTTAC 1446

Qy 101 GIYGLY----- 102

Dbb 1447 GGAGCGGACATGAGACAAACGCTTTTAAAATGCCATGCCATGGCGGGGCTGGACCG 1506

Qy 102 ----- 102

Dbb 1507 TGCCCCCTCCTCTCAGACAGACACCGAGCGGCTTACCCCACCTCTCCAGCGTTCCA 1586

Qy 103 -----ValValTYrGlnGluProValTYrGIYASnLys 113
|||:::

Dbb 1567 CCACCTTCTGTCCGTTGCTTCCAGGGTCGTGTATCAGATGATTTTATGATGCTGAG 1626

Qy 114 LeuLeuGlnGIYGLYTYrAlaAlaTYrArgTYrAlaGlnProThrProAlaThrAlaAla 133
:::|

Dbb 1627 ---ATTATGAGAGGTACGACGCTTACAGATACGTCGACCCGCT--GCAGCGCGGCA 1680

Qy 134 AlaTYrSerAspSerTYrGIYArGValIYr---AlaAlaAspProTYr 148
|||||

Dbb 1681 GCCTACAGCGACAGATTACGCGAGGCTTACGACGAGCTGCCGACCCGTAC 1728

RESULT 4
US-10-094-749-287
Sequence 287, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: MAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 08435/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 287

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: LENGTH: 1558
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-094-749-287
Alignment Scores:
Pred. No.: 6,42e-42 Length: 1558
Score: 430.50 Matches: 98
Percent Similarity: 63.69% Conservative: 9
Best Local Similarity: 58.33% Mismatches: 37
Query Match: 54.08% Indels: 25
Gaps: 6
US-09-809-545A-2_COPY_1_148 (1-148) x US-10-094-749-287 (1-1558)
QY 1 MetThAsnLysIbYsAlaValAsnProTYrThAsnGIYrPlybLeuAsnProValVal 20
Db 854 ATGACCAATTAAGAAGATGATCACACCACTATGCAAAATGTTGAATTAAGCCAGTAGTT 913
QY 21 GYAlAAlaAlYrSerProAspPheTYrAla----- 30
Db 914 GGAAGCTGTAATATGGTCTCGAGATATATATGACAGCATTCAGCTTTCAAGACATGTCCCTTA 973
QY 31 GYrThr-ValLeuLeuCYsGIuAlaAsnGIuGIYSerSerMetYrSerGIYProSe 50
Db 974 GGCAGATATGACAGACAGTCCCTCATTCAGAAAGGGGGTATCAACTTACATT-CCT-- 1030
QY 50 rSerLeuValTYrThrSerAlaMetProGIYpneProTYrPro--AlaAlaThrAlaAl 69
Db 1031 ----TTATATCAGTCTCCCTTATAGTCTTGCTTGCTTCCCTTACCTTACGACCCACAGCGC 1086
QY 69 aaAlaAlaTYrArgGIYAlaHisLeuATrGIYArgGIYArgThrValTYrAsnThrPheAr 89
Db 1087 AGCGGCTTTAGAGGAGCCCATTTGAGGGGCGAGGGCGACAGTATATGCTGACGTCCG 1146
QY 89 gaAlaAlaAlaProProProProIleProAlaTYrGIYGIYValValTYrGIuGIuProVa 109
Db 1147 A--GGGTAACCTTCAACAGCATCCCCGCTTATCCAGGTGTGTATTCAGACAGCGATT 1203
QY 109 lTYrGIYAsnLysLeuLeuGIuGIYTYrAlaAlaTYrArgTYrAlaGIuProThrPr 129
Db 1204 TTAAGGTGTGAC---CTTATAGGTGATATGACGCTTACAGATATCACAGCGCTGTAC 1260
QY 129 oAlaThr-----AlaAlaAlaTYrSerAspSerTYrGIYAr 141
Db 1261 TGCAACCGACGACCCGCTGTGACGCCGTGACGCCGCTTACGTTACGTTATATGGCAG 1320
QY 141 gValTYrAlaAlaAspProTYr 148
Db 1321 GGTGTACACAGCGACCCCTTAC 1342
RESULT 5
US-10-359-385-5
Sequence 5, Application US/10359385
Publication No. US20030143622A1
GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Lu, Aina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PF-0611 US
: CURRENT APPLICATION NUMBER: US/10/359,385
: PRIOR FILING DATE: 2003-02-05
: PRIOR APPLICATION NUMBER: US/09/116,657
: PRIOR FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA

```

ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 1250374
US-10-359-385-5

Alignment Scores:

Pred. No.: 9.38e-36 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: 13 Gaps: 6

US-09-809-545a-2_copy_1_148 (1-148) x US-10-359-385-5 (1-1506)

QY 1 MetThrAnlyYsAlaValAsnProTyrThrAnlyTTrpYsLeuAsnProValVal 20
DB 768 ATGACCAATAGAGAGATGTCACACCATATGCAATATGTTGAAATTAAGCCGATGTT 827
QY 21 G1ValAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAlaAsn--- 39
DB 828 GGAGCTGATATGTTGCTCGGAGTTATATGACATTCACAGCTTTCACAGCATGTGCTCTTA 887
QY 40 ---GlnGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
DB 888 GGCAATGATGACAGATGCCCCCTATCAGGAAGGGGATATCAACACTTACATTCCTTTA 947
QY 57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
DB 948 ATCATCTTCTGCTTCCCTTACCTTACCTGACGCCACCGAGCGCTTTCAGAGGAGCC 1007
QY 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaProProPro 95
DB 1008 CATTGAGGGGCAAGGGCGGACGATATGTCAGTCCGA---GGCGTACCTCCACACA 1064
QY 96 ProIleProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAsnYsLeuLeu 115
DB 1065 GCCATCCCCCGCTATCC----- 1081
QY 116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
DB 1082 AGGCGTGAATATGACGCTTACAGATATGCAACAGCTCTGACACCGCAGCCGCT 1141
QY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
DB 1142 GCTGACGCGCTGACGCGCTTACAGTGAAGCGTTATGCGAGGGTGAACAGCCGACCC 1201
QY 148 Tyr 148
DB 1202 TAC 1204

RESULT 6

US-10-104-047-659
Sequence 659, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104_047
CURRENT FILING DATE: 2002-03-25
PRIORITY APPLICATION NUMBER:
PRIORITY FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 659
LENGTH: 2397
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-659

Alignment Scores:

Pred. No.: 3.62e-07 Length: 2397

Score: 143.00 Matches: 30
Percent Similarity: 68.89% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 6
Query Match: 17.96% Indels: 8
DB: 12 Gaps: 1

US-09-809-545a-2_copy_1_148 (1-148) x US-10-104-047-659 (1-2397)

QY 112 AsnYsLeuLeuGlnGlnGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
DB 2058 TCCTCTCTCTCTGATGAGTGAATATGACGCTTACAGATATGCAACAGCTGCTACTGCAACC 2117
QY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyr 143
DB 2118 GCAGCAGCCGCTGCTGACGCGCTTACAGTGAACGTTATGCGAGGTTGATC 2177
QY 144 AlaAlaAspProTyr 148
DB 2178 ACAGCCGACCCCTTAC 2192

RESULT 7

US-09-974-300-1655
Sequence 1655, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:

APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: Expression
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIORITY APPLICATION NUMBER: 09/680,598
PRIORITY FILING DATE: 2000-10-06
PRIORITY APPLICATION NUMBER: 60/279,526
PRIORITY FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1655
LENGTH: 657
TYPE: DNA
ORGANISM: Bacillus licheniformis
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(657)
OTHER INFORMATION: n = A,T,C or G
US-09-974-300-1655

Alignment Scores:

Pred. No.: 0.055 Length: 657
Score: 94.00 Matches: 38
Percent Similarity: 40.15% Conservative: 17
Best Local Similarity: 27.74% Mismatches: 58
Query Match: 11.81% Indels: 24
DB: 10 Gaps: 8

US-09-809-545a-2_copy_1_148 (1-148) x US-09-974-300-1655 (1-657)

QY 2 ThrAsnYsLeuAlaValAsnProTyrThrAnlyTTrpYsLeuAsnProValValGly 21
DB 100 ACAAAAAAAAAAACCAATTAAACA---ACCAGGGGCTTAAACAAACGAAACCGGTAACTCC 156
QY 22 -----AlaValTyrSerProAspPhe---TyrAlaGlyThrValLeuLeu 35
DB 157 TTAACGCCCCCCCCGGGCTTTTTCACAGATTTCTTATACAAAACCTGGGCTTCTT 216
QY 36 CySGlnAlaAsnGlnGlnGlySerSerMetTyrSerGlyProSerSerLeuValTyrThr 55
DB 217 ACACCAAAAAAAAAACAGAGTCCGGTTTC-----CCCTTAAGGAAAAATTAAAC 267
QY 56 SerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyrArgGlyAla 75
DB 268 CCCTTAAACCAATTCAACTTTTAACTTTAAACGCAACCCCAATCCCAACCCCTC 327

[illegible][illegible]

```
OY 81 -----GlyArgThrValTyrAsnThrPheArgAlaIleAlaIleProProP 95
DB 312 TGGTCCCCCTGACCCGGGACACCTCTCCACGACCATCTCGAATGTCCCTCTCC 371
OY 95 oProIleProAlaTyrGlyVal-----Val-TyrGlnGluProValTyrGlyA 112
DB 372 TCCAGGCCCTTCTTACAGTGGGGTCTCTGGAATGTCTTCCCAAAACCATCTACGCA 431
OY 112 snLys-LeuLeuGlnGlyGlyTyrAlaIleTyrArgTyrAlaGlnProThrProAlaThr 131
DB 432 ATCTGTCTTCCGAGCC-----CCCACTCCAGCCCG 464
OY 132 Ala 132
DB 465 GCA 467

RESULT 10
US-10-027-632-24832
; Sequence 24832, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24832
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24832

Alignment Scores:
Pred. NO.: 0.0899 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-027-632-24832 (1-699)
OY 25 SerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAla-AbsnGlnGlySerse 44
DB 84 ACACCAAGACAGAGCGGGTCTCATCTCTCTGCTGTGCTTCA-----YCTGG 134
OY 44 tMeTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
DB 135 ACAAGTCTCAGGCCCGCCAGCATCTC---CAGGWAAGACCCAGGCGCTGCTCTTACCA 191
OY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgG 74
DB 192 CTGACCTCACAAGTCTCTCCCAAGTGCAGCTCCACCTCTCTCTGCCCCAGAGG 251
OY 74 yAlaHleValLeuArgGlyArg----- 80
```

```
DB 252 AGAARACCTAAATCAAAATCTCCAACTGATAGAGGTACAGACTCTTGCCCTTCC 311
OY 81 -----GlyArgThrValTyrAsnThrPheArgAlaIleAlaIleProProP 95
DB 312 TGGTCCCCCTGACCCGGGACACCTCTCCACGACCATCTCGAATGTCCCTCTCC 371
OY 95 oProIleProAlaTyrGlyVal-----Val-TyrGlnGluProValTyrGlyA 112
DB 372 TCCAGGCCCTTCTTACAGTGGGGTCTCTGGAATGTCTTCCCAAAACCATCTACGCA 431
OY 112 snLys-LeuLeuGlnGlyGlyTyrAlaIleTyrArgTyrAlaGlnProThrProAlaThr 131
DB 432 ATCTGTCTTCCGAGCC-----CCCACTCCAGCCCG 464
OY 132 Ala 132
DB 465 GCA 467

RESULT 11
US-10-027-632-24830
; Sequence 24830, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24830
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24830

Alignment Scores:
Pred. NO.: 0.0899 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-027-632-24830 (1-699)
OY 25 SerProAspPheTyrAlaGlyThrValLeuLeuCySGlnAla-AbsnGlnGlySerse 44
DB 84 ACACCAAGACAGAGCGGGTCTCATCTCTCTGCTGTGCTTCA-----YCTGG 134
OY 44 tMeTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
DB 135 ACAAGTCTCAGGCCCGCCAGCATCTC---CAGGWAAGACCCAGGCGCTGCTCTTACCA 191
OY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgG 74
DB 192 CTGACCTCACAAGTCTCTCCCAAGTGCAGCTCCACCTCTCTCTGCCCCAGAGG 251
```

```

QY 74 yAlaHisLeuArgGlyArg----- 80
Db 252 AGAARACCTAAATCGAATCTCCAGCTGATAGAGATACAGAGCTTGGCTTCC 311
QY 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaProProPr 95
Db 312 TGTGCCCCCTGACCCGGGACACCTCTCCACAGCATGTGAGATGTCCTCTCC 371
QY 95 oProIleProAlaTyrGlyGlyVal-----Val-TyrGlnGluProValTyrGlyA 112
Db 372 TCCAGGCCCTTCTTACAGTGGGGTCTCTCGAATGTCTTCCAAACCATCTACGCA 431
QY 112 snlys-LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
Db 432 ATCTGCTCTTCGAGGC-----CCAGTCCAGGCCCG 464
QY 132 Ala 132
Db 465 GCA 467

```

RESULT 12

```

US-10-027-632-24831
; Sequence 24831, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24831
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24831

```

Alignment Scores:

```

Pred. No.: 0.0899 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
DB: 14 Gaps: 6

```

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-027-632-24831 (1-699)

```

QY 25 SerProAspPheTyrAlaGlyThrValLeuLeuCyGlnAla-AsnGlnGluGlySerse 44
Db 84 ACACCAAGACAGAAACGGGGTCTCAATCCCTCTGCTGCTGCTCA-----YCTGG 134
QY 44 rmetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
Db 135 ACAAGTCTCAGGCCCGCCAGCATCTC---CAGGWAAGACCAAGGGCTCTGCTCTTACCA 191
QY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgG 74
Db 192 CTGACCTCACCAGTCTCTCCCAAGTGCAGGCTTCACCTCTCTCTGCCCCAGAGG 251

```

```

QY 74 yAlaHisLeuArgGlyArg----- 80
Db 252 AGAARACCTAAATCGAATCTCCAGCTGATAGAGATACAGAGCTTGGCTTCC 311
QY 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaProProPr 95
Db 312 TGTGCCCCCTGACCCGGGACACCTCTCCACAGCATGTGAGATGTCCTCTCC 371
QY 95 oProIleProAlaTyrGlyGlyVal-----Val-TyrGlnGluProValTyrGlyA 112
Db 372 TCCAGGCCCTTCTTACAGTGGGGTCTCTCGAATGTCTTCCAAACCATCTACGCA 431
QY 112 snlys-LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
Db 432 ATCTGCTCTTCGAGGC-----CCAGTCCAGGCCCG 464
QY 132 Ala 132
Db 465 GCA 467

```

RESULT 13

```

US-10-027-632-24832
; Sequence 24832, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24832
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24832

```

Alignment Scores:

```

Pred. No.: 0.0899 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
DB: 14 Gaps: 6

```

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-027-632-24832 (1-699)

```

QY 25 SerProAspPheTyrAlaGlyThrValLeuLeuCyGlnAla-AsnGlnGluGlySerse 44
Db 84 ACACCAAGACAGAAACGGGGTCTCAATCCCTCTGCTGCTGCTCA-----YCTGG 134
QY 44 rmetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
Db 135 ACAAGTCTCAGGCCCGCCAGCATCTC---CAGGWAAGACCAAGGGCTCTGCTCTTACCA 191
QY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgG 74

```

Db 192 CTGACCTCACCAAGTCCCTCCCAAGTGCAGCCTCCACCTCTCTCCCTTGCCAGAG 251
Qy 74 yAlaHisLeuArgGlyArg----- 80
Db 252 AGAARACCTTAATAATCGAAATCTCCACGTGATAGAGTACAGATCTTGAGCCTTCC 311
Qy 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaIleProProP 95
Db 312 TGGGCCCCCTGACCGGGGACACCTCTCCACAGACCATGTCTGATGTCCTCCCTCC 371
Qy 95 oProlleProAlaTyrGlyGlyVal-----Val-TyrGlnGluProValTyrGlyA 112
Db 372 TCCAGGCTCTTCTTACAGTGGGGTCTCTGGAATGCTCTTCCCAACCATCTACCCAA 431
Qy 112 enlys-leuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
Db 432 ATCCTGCTCTTCCGAGGC-----CCCACTCCAGCCCG 464
Qy 132 Ala 132
Db 465 GCA 467

RESULT 14

US-10-301-822-25
; Sequence 25, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: PM001-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(9192)
US-10-301-822-25

Alignment Scores:

Pred. No.: 2.95 Length: 11447
Score: 92.50 Matches: 28
Percent Similarity: 39.22% Conservative: 12
Best Local Similarity: 27.45% Mismatches: 41
Query Match: 11.62% Indels: 21
DB: 13 Gaps: 4

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-301-822-25 (1-11447)

Qy 50 SerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAla 69
Db 6232 AACATATGAATATGACAGCCCTGCACACCTGACACTCAATAT---AAAATTACTGTTATT 6288
Qy 70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyArgGlyArgThrVal----- 84

Db 6289 GCTGTATTAGAGATGAGATGAGTGGCCATCTAACAGAAATGGAAGAACTGGGACTC 6348
Qy 85 -----TyrAsnThrPheArgAlaAla 92
Db 6349 CTTCCTCTCCAGAACATACATCTCTGACGAATGATATACAGATTCAGGGTCTCTGG 6408
Qy 93 ProProProProlleProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAsn 112
Db 6409 GATCCTTCAACCTCTCCAGTCTTGATATATAAATAGTATATATAGCCAGTGGGTTCCAA 6468
Qy 113 lysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro 129
Db 6469 GAGCCCATGGAACCTTGTGTGGAGAAATGACATCATATACCTTACACATCTCAATCC 6528
Qy 130 AlaThr 131
Db 6529 AGCACC 6534

RESULT 15

US-10-177-293-60
; Sequence 60, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Ganavarrpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoerach, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegül
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-60

Alignment Scores:

Pred. No.: 2.95 Length: 11447
Score: 92.50 Matches: 28
Percent Similarity: 39.22% Conservative: 12
Best Local Similarity: 27.45% Mismatches: 41
Query Match: 11.62% Indels: 21

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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2004, 08:41:56 ; Search time 48,9117 Seconds
(without alignments)
1335.564 Million cell updates/sec

Title: US-09-809-545a-2_COPY_1_148

Perfect score: 796

Sequence: 1 MTNRKAVNPYINGMKLNPV.....PATAAASPSYGRVYADPY 148

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rnt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09809545 @CGN 1 1 133 @runtat_15012004_061051_2480 -NCP=6 -ICU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-BEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued Patents NA:*
- 1: /cg2_6/prodata/2/ina/5A_COMB.seq:*
 - 2: /cg2_6/prodata/2/ina/5B_COMB.seq:*
 - 3: /cg2_6/prodata/2/ina/6A_COMB.seq:*
 - 4: /cg2_6/prodata/2/ina/6B_COMB.seq:*
 - 5: /cg2_6/prodata/2/ina/6C_COMB.seq:*
 - 6: /cg2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	674	84.7	2372	3	US-09-145-391-1
2	379	47.6	1506	4	US-09-176-657-5
3	379	47.6	1506	4	US-09-421-299-5
4	93	11.7	914	2	US-08-935-450-10
5	92.5	11.6	28958	1	US-08-258-261B-6
6	92.5	11.6	28958	1	US-08-456-837-6
7	92.5	11.6	28958	1	US-08-457-342-6
8	92.5	11.6	28958	1	US-08-457-342-6
9	92.5	11.6	28958	1	US-08-458-076A-6
10	92.5	11.6	28958	1	US-08-764-233A-4
11	92.5	11.6	28958	1	US-08-457-335A-6
12	92.5	11.6	28958	1	US-08-729-214-6

13	92.5	11.6	28958	3	US-09-028-934-6	Sequence 6, Appli
14	92.5	11.6	49377	1	US-08-764-233A-1	Sequence 1, Appli
15	91	11.4	821	3	US-08-990-823-62	Sequence 62, Appli
16	91	11.4	821	4	US-09-477-135A-62	Sequence 62, Appli
17	91	11.4	1896	4	US-09-343-011B-4	Sequence 4, Appli
18	89.5	11.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
19	89.5	11.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
20	87.5	11.0	3231	1	US-08-195-152-1	Sequence 1, Appli
21	86.5	10.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
22	86.5	10.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
23	85.5	10.7	1140	3	US-09-023-173-4	Sequence 4, Appli
24	85.5	10.7	2208	3	US-09-620-312D-502	Sequence 502, App
25	85	10.7	53526	3	US-08-658-136-2	Sequence 2, Appli
26	85	10.7	53577	3	US-08-658-136-1	Sequence 1, Appli
27	84.5	10.6	1462	1	US-08-552-142A-16	Sequence 16, Appli
28	84.5	10.6	1494	3	US-09-255-502-1	Sequence 1, Appli
29	84.5	10.6	1496	6	RE34606-1	Patent No. RE34,60
30	84.5	10.6	1497	1	US-08-322-677A-6	Sequence 6, Appli
31	84.5	10.6	1497	1	US-08-322-676-6	Sequence 6, Appli
32	84.5	10.6	1497	3	US-08-898-218-6	Sequence 6, Appli
33	84.5	10.6	1497	3	US-08-848-793-6	Sequence 6, Appli
34	84.5	10.6	1497	4	US-09-445-270-1	Sequence 1, Appli
35	84.5	10.6	1497	4	US-09-178-173A-1	Sequence 1, Appli
36	84.5	10.6	1497	4	US-08-322-678-6	Sequence 6, Appli
37	84.5	10.6	1497	6	5472855-1	Patent No. 5472855
38	84.5	10.6	1513	4	US-09-178-155-1	Sequence 1, Appli
39	84.5	10.6	1868	1	US-08-069-863-1	Sequence 1, Appli
40	84.5	10.6	1868	1	US-08-309-069-1	Sequence 1, Appli
41	84.5	10.6	1868	1	US-08-562-833-1	Sequence 1, Appli
42	84.5	10.6	1868	4	US-09-659-749-1	Sequence 1, Appli
43	84.5	10.6	1868	4	US-09-672-105-1	Sequence 1, Appli
44	84.5	10.6	1868	5	PCR-US95-05520-1	Sequence 1, Appli
45	83.5	10.5	1352	1	US-08-552-142A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-145-391-1
; Sequence 1, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Polster, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins.
; FILE REFERENCE: CB 3093
; CURRENT APPLICATION NUMBER: US/09/145,391
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (987)..(1979)
US-09-145-391-1

Alignment Scores:
Pred. No.: 4,266-59
Score: 674.00
Percent Similarity: 83.23%
Best Local Similarity: 81.44%
Query Match: 84.67%
DB: 3
Gaps: 2

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-145-391-1 (1-2372)

Qy 1 MetThrAnLysLysAlaValAsnProTyrThrAnGlyTTPLYsLeuAsnProValVal 20
Db 1572 ATGACAAATATAAAGACCGCTCAACCTTATACAAATGCTGGAATTCACACTGTG 1631

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QY      21  G|VAlaValTyrSerProaepheTyrAlaG|YThrValIleuLeuCyGlnAlaAsnGln 40
Db      1632 GGGGAGTCTTACAGTCCCGAATTCATGACAGGAGCTCTGTTGGCCAGGCCACAG 1691
QY      41  GluG|YSerSermetTyrSerG|YProSerSerIeuValTyrThrSerAlaMetProG|Y 60
Db      1692 GAGGAGTCTTCATGATGACATGCGCCCGCATCTTATATACCTTCTGCATAGCCAGGC 1751
QY      61  PheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgG|YAlaHisIeuAlaArgG|YArg 80
Db      1752 TTCCCGATCCAGAGCAGCCGCGCGCCGCTTACGAGGGGGCGACCTCCAGCGCCGC 1811
QY      81  G|YArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProlIeuProAlaTyr 100
Db      1812 GGTGCGACCGGTGACACACCTTCAGGGCGCGCGCCCGCCCGCCCGCATCCGCGCTAC 1871
QY      101  G|YG|YValValTyr-G|ngIuProValTyrG|YAsnIleuLeuGlnG|YAla 120
Db      1872 GGGGCTTCTTTTACCAGATGATTTTATGTCAGAC---ATTATGCTGTTATGC 1928
QY      120  aa|a|TyrArgTyrAlaGlnProThrProAlaThrAlaAlaAlaTyrSerAspSer----- 138
Db      1929 TGCATACCGCTACGCCAGCCTACCTCGCACCTGCGCTACAGTACAG-AAATC 1987
QY      139  -----TyrG|YArgVa 142
Db      1988 AGTTCGCTCTGCTGACGACAGTAAATTTCTGTAAACCTTCGACGTTACGAGCAGT 2047
QY      142  1TyrAlaAlaAspProTyr 148
Db      2048 TTATGCTGCCGACCCCTAC 2066
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RESULT 2

```
US-09-176-657-5
; Sequence 5, Application US/09176657
; Patent No. 6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176,657
; CURRENT FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-176-657-5
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Alignment Scores:

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Pred. No.: 1,92e-29 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: 3 Gaps: 6
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US-09-809-545a-2_COPY_1_148 (1-148) x US-09-176-657-5 (1-1506)

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QY      1  MetThrAsnIleValAlaValAsnProTyrThrAsnG|YTrpIleuAsnProValVal 20
Db      768 ATGACCAATAGAGAGATGCTCACACCATATGCAATGTTGGAAATTAAGCCAGTATT 827
QY      21  G|VAlaValTyrSerProaepheTyrAlaG|YThrValIleuLeuCyGlnAlaAsn--- 39
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Db      828 GAGGCTGATATAGTCCGAGATTATATGACGATCCAGCTTTCACACAGATGTGCTCA 887
QY      40  ---G|ngIuG|YSerSermetTyrSerG|YProSerSerIeu-----ValTyrThrSer 56
Db      888 GGCATATGACGACATGCTCCCTATGAGAAAGGGGGTATCAACCTTACATTCCTTTA 947
QY      57  AlaMetProG|YPheProTyrPro---AlaAlaThrAlaAlaAlaAlaTyrArgG|YAla 75
Db      948 ATCATTCCTGGCTTCTCCCTTACCTTACGACGACACAGCGCGCTTTCAGAGAGGCC 1007
QY      76  HisIeuArgG|YArgG|YArgThrValTyrAsnThrPheArgAlaAlaAlaProPro 95
Db      1008 CATTGAGGGGCGAGAGGGCGGACAGTATATGTGTCAGTCCGA---GCGGTACCTCCACAA 1064
QY      96  ProlIeuProAlaTyrG|YValValValTyrG|ngIuProValTyrG|YAsnIleuLeu 115
Db      1065 GCCATCCCGCTTATC----- 1081
QY      116  G|ngIuG|YTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
Db      1082 AGGGGTGATATGACACCTTACAGATATGACAGCCTGCTTACGACCGGACCGCT 1141
QY      132  -----AlaAlaAlaTyrSerAspSerTyrG|YArgValTyrAlaAlaAspPro 147
Db      1142 GCTGACCGCGCTGACGCGCTTACAGTGAAGTTATGAGAGGGGTATACACAGCGACCC 1201
QY      148  Tyr 148
Db      1202 TAC 1204
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RESULT 3

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US-09-421-299-5
; Sequence 5, Application US/09421299
; Patent No. 6524579
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/421,299
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: 09/176,657
; EARLIER FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-421-299-5
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Alignment Scores:

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Pred. No.: 1,92e-29 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: 4 Gaps: 6
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US-09-809-545a-2_COPY_1_148 (1-148) x US-09-421-299-5 (1-1506)

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QY      1  MetThrAsnIleValAlaValAsnProTyrThrAsnG|YTrpIleuAsnProValVal 20
Db      768 ATGACCAATAGAGAGATGCTCACACCATATGCAATGTTGGAAATTAAGCCAGTATT 827
QY      21  G|VAlaValTyrSerProaepheTyrAlaG|YThrValIleuLeuCyGlnAlaAsn--- 39
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DB 828 GGAGCTGATATATGTCGGAGTTATATGACATCCAGCTTTACAGACATGTGTCCCTTA 887
 40 ---GlnGlnGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
 DB 888 GCGAATGATCAGCAGAGCGCCCTATACAGAGAGGGGGATTCACAACCTTATCCCTTA 947
 57 AlameProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaAlaTyrArgGlyAla 75
 DB 948 ATGATTCCTGCTTCCCTTATCCCTTACGACGACCAACCGCAGCCGCTTTCAGAGAGCC 1007
 76 HisLeuArgGlyArgGlyValArgThrValTyrAsnThrPheArgAlaAlaAlaProPro 95
 DB 1008 CATTGAGGGGAGAGGGCGACAGATATGTCAGTCCGA---CGGTACCTCCACAAC 1064
 96 ProIleProAlaTyrGlyGlyValValTyrGlnGlnProAlaTyrGlyAsnLysLeuLeu 115
 DB 1065 GCCATCCCGCGCTATCC----- 1081
 116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
 DB 1082 AGGGGTGATATGACGCTTACAGATATGCAACGCTGCTACTGCAACCGCAGCCGCT 1141
 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAlaPro 147
 DB 1142 GCTGACGCCGCTCAGCGCTTACAGTACGATTATGCGGGGTGTACACAGCCGACCC 1201
 148 Tyr 148
 DB 1202 TAC 1204

RESULT 4

US-08-935-450-10
 ; Sequence 10, Application US/08935450
 ; Patent No. 5977311
 ; GENERAL INFORMATION:
 ; APPLICANT: Nandabalan, Krishnan
 ; APPLICANT: Yang, Meijia
 ; APPLICANT: Schulz, Vincent
 ; TITLE OF INVENTION: 53BP2 COMPLEXES
 ; FILE REFERENCE: 7934-054
 ; CURRENT APPLICATION NUMBER: US/08/935,450
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 914
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-08-935-450-10

Alignment Scores:

Pred. No.:	1	Length:	914
Score:	93.00	Matches:	39
Percent Similarity:	41.38%	Conservative:	9
Best Local Similarity:	33.62%	Mismatches:	42
Query Match:	11.68%	Indels:	26
DB:	2	Gaps:	5

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-935-450-10 (1-914)

QY 24 TysSerProkSerPheTyrAlaGlyThrValLeuLeuGlnAlaGlnGlnGlySer 43
 DB 230 TACAGCCCT-----GCTGGAAACCCCGAGGGCC 259
 44 SerMetTyrSerGlyProSerSerLeuValTyrThrSerAla-MetProGlyPheProTyr 63
 DB 260 AGACCTACATATGAAAGACACATCCCTGCTCAAGCCCAATACAGACCCACCC 319
 63 rProAlaAlaThrAla-----AlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 81
 DB 320 GTGAGAGCTAAGCCCTTTCACAGCCGAGTTACAGCCACCACTTAC---AACAGAG 376

QY 81 YArgThrValTyrAsnThrPheArgAlaAlaAla-ProProProIleProAlaTyrG 101
 DB 377 GAGTTTACAGCAGAGGTTTACACAGGCCACCGCTTCCACTCCACACACCTGCTTCA 436
 101 LysGlyValValTyrGlnGlnProValTyrGlyAsnLysLeuLeuGlnGlyTyrAla 121
 DB 437 AC-----TATGGAGC-----TACGGGGTTCAACC 463
 121 LaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaAlaTyr 135
 DB 464 CGGCCCTTATACCCACCGCCACCCCGCCACCGCAGACCTTAC 507

RESULT 5

US-08-258-261B-6
 ; Sequence 6, Application US/08258261B
 ; Patent No. 5639949
 ; GENERAL INFORMATION:
 ; APPLICANT: Schnupp, Thomas
 ; APPLICANT: Ligou, James M.
 ; APPLICANT: Beck, James Joseph
 ; APPLICANT: Hill, Dwight Steven
 ; APPLICANT: Ryals, John Andrew
 ; APPLICANT: Gaffney, Thomas Deane
 ; APPLICANT: Lam, Stephen Ting
 ; APPLICANT: Hammer, Phillip E.
 ; APPLICANT: Uknes, Scott Joseph
 ; TITLE OF INVENTION: Genes for the synthesis of
 ; TITLE OF INVENTION: antipathogenic substances
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ciba-Geigy Corporation
 ; STREET: 7 Skyline Drive
 ; CITY: Hawthorne
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10532

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/258,261B
 ; FILING DATE: 08-JUN-1994
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/457,205
 ; FILING DATE: 01-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bimer, James Scott
 ; REGISTRATION NUMBER: 36,129
 ; REFERENCE/DOCKET INFORMATION:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 919-541-8614
 ; TELEFAX: 919-541-8689
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28958 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO

Alignment Scores:

Pred. No.:	106	Length:	28958
Score:	92.50	Matches:	34
Percent Similarity:	41.28%	Conservative:	11
Best Local Similarity:	31.19%	Mismatches:	52
Query Match:	11.62%	Indels:	12
DB:	1	Gaps:	4


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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-457-342-6
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Alignment Scores:
Pred. No.: 106          Length: 28958
Score: 92.50          Matches: 34
Percent Similarity: 41.28%      Conservative: 11
Best Local Similarity: 31.19%   Mismatches: 52
Query Match: 11.62%           Indels: 12
DB: 1                      Gaps: 4
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US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-342-6 (1-28958)

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QY 47 SerGlyProSerSerLeuValTyThrSerAlaMetProGlyPheProTyRProAlaAla 66
DB 10706 AGCGGCTCTCCGACGATGGGCGATCGCTTCCGTCGAGGTCAGCCCACTCCGCTCTCA 10765
QY 67 ThrAlaAlaAlaAlaTyR--ArgGlyAlaHis-LeuArgGlyAArgGlyAArgThValTy 85
DB 10766 CGCTCCGCTCCGCGAGACCTGGAGGCGCTCACCGCTCGATCCGCTGCTGGGCTCCA 10825
QY 85 rAntThrPheArgAlaAlaAlaProProProProleProAlaTyRgLyValTyRAl 105
DB 10826 TTCGACG--AGAGAGAGGCGACCTCCGCGCTGCTCTCTCTGGGCGAGCTCTCTA 10882
QY 105 rGlnGluProValTyRgLyAsnLyLeuGlnGlyTyRAlaAlaTyRgTyRAl 125
DB 10883 CCGGAGGCT-----CGCGCTCGACTGGAGGAGCTTCTTCGCGCCCTACGCTCCCC 10933
QY 125 agIn-----ProThrProAlaThrAlaAlaAlaTyRserAspSerTy 139
DB 10934 GCAAGGCTCTCCCTCCCACTACCTCCCTTCACGAGAGAGCGGTTCTGGCTCGAGCTCCA 10993
QY 139 rGlyAArgValTyRAlaAlaAspPro 147
DB 10994 CGGACGAAAGCTTCGACGCTGCT 11018

RESULT 8
US-08-457-646a-6
Sequence 6, Application US/08457646a
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
```

```

APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,646a
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-457-646a-6

Alignment Scores:
Pred. No.: 106          Length: 28958
Score: 92.50          Matches: 34
Percent Similarity: 41.28%      Conservative: 11
Best Local Similarity: 31.19%   Mismatches: 52
Query Match: 11.62%           Indels: 12
DB: 1                      Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-646a-6 (1-28958)

QY 47 SerGlyProSerSerLeuValTyThrSerAlaMetProGlyPheProTyRProAlaAla 66
DB 10706 AGCGGCTCTCCGACGATGGGCGATCGCTTCCGTCGAGGTCAGCCCACTCCGCTCTCA 10765
QY 67 ThrAlaAlaAlaAlaTyR--ArgGlyAlaHis-LeuArgGlyAArgGlyAArgThValTy 85
DB 10766 CGCTCCGCTCCGCGAGACCTGGAGGCGCTCACCGCTCGATCCGCTGCTGGGCTCCA 10825
QY 85 rAntThrPheArgAlaAlaAlaProProProProleProAlaTyRgLyValTyRAl 105
DB 10826 TTCGACG--AGAGAGAGGCGACCTCCGCGCTGCTCTCTCTGGGCGAGCTCTCTA 10882
QY 105 rGlnGluProValTyRgLyAsnLyLeuGlnGlyTyRAlaAlaTyRgTyRAl 125
DB 10883 CCGGAGGCT-----CGCGCTCGACTGGAGGAGCTTCTTCGCGCCCTACGCTCCCC 10933
QY 125 agIn-----ProThrProAlaThrAlaAlaAlaTyRserAspSerTy 139
DB 10934 GCAAGGCTCTCCCTCCCACTACCTCCCTTCACGAGAGAGCGGTTCTGGCTCGAGCTCCA 10993
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QY      139    rglArqValtyrAlaIalaaePro 147
          |||||
Db       10994 CGACGAAAGCTTCCGACGTGGCCT 11018

RESULT 9
US-08-458-076A-6
Sequence 6, Application US/08458076A
Patent No. 5698425
GENERAL INFORMATION:
APPLICANT: Schnupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
NUMBER OF INVENTION: antipathogenic substances
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Gelgy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,076A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-458-076A-6

Alignment Scores:
Pred. NO.:           106              Length:     28958
Percent:             92.50            Matches:     34
Score Similarity:    41.28%           Conservative: 11
Best Local Similarity: 31.19%         Mismatches:  52
Query Match:         11.62%           Indels:      12
DB:                  1                Gaps:        4

US-09-809-545A-2_COPY_1_148 (1-148) x US-08-458-076A-6 (1-28958)

QY      47    SerclgYProBserSerLeuValTyThSeriIaaMeCrProDlySheProTYrPrroIaaIa 66
          ||||| | |
          |||||||
          |||
          |||
          :::
```

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Db      10706 AGGGGCTCCCTGCAGCAGTGGGCAGTCGTTCCCGTCGAGGTCAGGCCCCATCCCGTGCCTCA 107655
Oy      67  ThrAlaAlaAlaAlaTyr---ArgIylAlaHis-LeuArgIylAArgIylArgThyValTy 85
Db      10766 CGCGTCGCCCTCCCGAGACCTCGGACCGGTCAACCGCTGCATCCCGTCGTGGCGGTCCCA 108255
Oy      85  rAanThrPheArgAlaAlaAlaProProProProlleProAlaTyrGlyIylValValTy 105
Db      10826 TTCACGCG--AGAAAGAGGCCACCTCGCCCGCGCTGCTCTCTTCCTGGGGGAGACTCTCTA 108822
Oy      105  rGIngluProValTyrGlyAsnIylAuleuIngInglIylTyrAlaAlaTyrArgTyrAl 125
Db      10883 CCGAGGCGCT-----CGCGCTCGACTGGAAAGACTTCTTCGCGGCCCTACGCTCCCC 109333
Oy      125  aGln-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTy 139
Db      10934 GCAAAGTCTCCCTCCGCCACCTACCTCCCTTCGAGGAGGCGGTTCTGGCTCGACGTCCTCA 109933
Oy      139  rGlyArgValTyrAlaAlaAlaAspPro 147
Db      10994 CGAGCGAAGCCTTCGACGTCGCTT 11018

RESULT 10
US-08-764-233A-4
; Sequence 4, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezana
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,233A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 1506/CIP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Sorangium cellulosum

```

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; IMMEDIATE SOURCE:
; CLONE: p98/1
US-08-764-233A-4

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-08-809-545A-2_COPY_1_148 (1-148) x US-08-764-233A-4 (1-28958)

QY 47 SerGlyProSerSerLeuValTyTrhSerAlaMetProGlyPheProTyProAlaAla 66
Db 10706 AGCGGCTCTCCGAGAGGAGCTCGAGGCGCTACCGCTGATCCCGTGTGTGGCTCA 10765
QY 67 ThrAlaAlaAlaTyTr---ArgGlyAlaHis-LeuArgGlyArgGlyValrghrValTy 85
Db 10766 CGCTGCGCTCCGAGAGCTCGAGGCGCTACCGCTGATCCCGTGTGTGGCTCA 10825
QY 85 rAsnThrPheArgAlaAlaAlaProProProlleProAlaTyrglyValValTy 105
Db 10826 TTCGACG---AGAGAGAGCGCACCTCCGCCCTGCTCTCTCTGGGGAGACTCTCA 10882
QY 105 rGlnGluProValTyTrGlyAsnlybLeuLeuGlnGlyTyTrAlaAlaTyTrGlyTrAl 125
Db 10883 CCCGAGGCGCT-----CGCGCTCGACTGGAAGGACTCTTCGGGCGCTACGCTCCCC 10933
QY 125 agln-----ProThrProAlaThrAlaAlaAlaTySerAspSerTy 139
Db 10934 GGAAGGTCCTCCCTCCCACTACCTTCCTCCAGCAGAGCGCTTCGGCTGACGCTCCA 10993
QY 139 rGlyArgValTyTrAlaAlaAspPro 147
Db 10994 CGAGCAGAACGCTTCCGACGTCCT 11018

RESULT 11
US-08-457-335A-6
; Sequence 6, Application US/08457335A
; Patent No. 5723759
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Ukens, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,335A
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205

```

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: FILING DATE: 01-JUN-1995
: APPLICATION NUMBER: 08/258,261
: FILING DATE: 08-Jun-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmer, James Scott
: REGISTRATION NUMBER: 36,129
: REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8614
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28958 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
US-08-457-335A-6

Alignment Scores:
Pred. No.: 106
Score: 92.50
Percent Similarity: 41.28%
Best Local Similarity: 31.19%
Query Match: 11.62%
DB: 1
Gaps: 4

US-09-809-545A-2_COPY_1_148 (1-148) x US-08-457-335A-6 (1-28958)

OY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
Db 10706 AGCGGCTCTCCGACGATGGCATCGCTTCTCCGTCGAGGTCAAGCCCCATCCCGTCTCA 107655
OY 67 ThrAlaAlaAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgThrValTyr 85
Db 10766 CGCTCGCCCTCCCGCGAGACCTGCGAGCGCTCACCGTCAATCCGTCGTCGCGGCTCA 108235
OY 85 rAsnThrPheArgAlaAlaAlaProProProProIleProAlaTyrGlyGlyValValTyr 105
Db 10826 TTCGAGC---AGAAGAGCGCACCTCGCCGCTGCTCTCTCCGCGGCGGAGCCTCTCA 108822
OY 105 rGlnGluProValTyrGlyAsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAl 125
Db 10883 CCGCAGGCGCT-----CGCGCTCGACTGGAGAGCACTTCGCGGCCCTACGCTCCCC 109333
OY 125 agIn-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTyr 139
Db 10934 GCAAGGCTCTCCCTCCCACTACCTACCTTCACAGGAGAGCGGTTCTGCGTCAAGCTCTCA 109933
OY 139 rGlyArgValTyrAlaAlaAspPro 147
Db 10994 CGGACGACGCTTCGACGTCGCT 11018

RESULT 12
US-08-729-214-6
: Sequence 6, Application US/08729214
: Patent No. 5817502
: GENERAL INFORMATION:
: APPLICANT: Ligon, James M.
: APPLICANT: Hill, Dwight Steven
: APPLICANT: Ryals, John Andrew
: APPLICANT: Hammer, Phillip B.
: APPLICANT: Van Pee, Karl-Heinz
: APPLICANT: Kirner, Sabine
: TITLE OF INVENTION: Genes for the synthesis of
: TITLE OF INVENTION: antipathogenic substances
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 520 White Plains Road
: CITY: Tarrytown

```

```
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,214
FILING DATE: TBA
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1506/CIP5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-729-214-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-729-214-6 (1-28958)
QY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
D 10706 AGCGGCTCTCGACGATGGGATCGCTTCTCCGTCGAGTCAGCCCCCATCCCGTGTCTCA 10765
QY 67 ThrAlaAlaAlaAlaTyr--ArgGlyAlaHis-LeuArgGlyValArgGlyValThrValTy 85
D 10766 CGCTCGCCCTCCGAGACCTCGAGCGGCTCTACCGCTCGATCCCGTGTGTGCGGCTCA 10825
QY 85 rAenThrPheArGAlaAlaAlaProProProProlleProAlaTyrGlyGlyValValTy 105
D 10826 TTCGACG--AGAGAAGGCCACCTCGCCCGCTGTCTCTCTCGGGCGGAGCTGTCTA 10882
QY 105 rGInGluProValTyrGlyValnlySLeuLeuGInGlyGlyTyrAlaAlaTyrArGTYrAl 125
D 10883 CCCGAGGCGCT-----CGCGCTCGACTGGAAGAGCTTCTTCGCCCGCTTACCGCTCC 10933
QY 125 agIn-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTy 139
D 10934 GCAAGGCTCTCCCTCCACCTACCTTCTTCAGCAGAGCGGTGTGCTGACGTCTCA 10993
QY 139 rGlyArGValTyrAlaAlaAerPro 147
D 10994 CGAGCGAAGCTTCCGACGTGCGCT 11018

RESULT 13
US-09-028-934-6
Sequence 6, Application US/09028934
Patent No. 6117670
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Lam, Steven T.
APPLICANT: Hammer, Philip E.
```

```
APPLICANT: van Pee, Karl-Heinz
APPLICANT: Kirner, Sabine
APPLICANT: Young, Thomas R.
TITLE OF INVENTION: Pyrolytic Biosynthesis Genes and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6117670artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,934
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1506/CIP7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-028-934-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-028-934-6 (1-28958)
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D 10706 AGCGGCTCTCGACGATGGGATCGCTTCTCCGTCGAGTCAGCCCCCATCCCGTGTCTCA 10765
QY 67 ThrAlaAlaAlaAlaTyr--ArgGlyAlaHis-LeuArgGlyValArgGlyValThrValTy 85
D 10766 CGCTCGCCCTCCGAGACCTCGAGCGGCTCTACCGCTCGATCCCGTGTGTGCGGCTCA 10825
QY 85 rAenThrPheArGAlaAlaAlaProProProProlleProAlaTyrGlyGlyValValTy 105
D 10826 TTCGACG--AGAGAAGGCCACCTCGCCCGCTGTCTCTCTCGGGCGGAGCTGTCTA 10882
QY 105 rGInGluProValTyrGlyValnlySLeuLeuGInGlyGlyTyrAlaAlaTyrArGTYrAl 125
D 10883 CCCGAGGCGCT-----CGCGCTCGACTGGAAGAGCTTCTTCGCCCGCTTACCGCTCC 10933
QY 125 agIn-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTy 139
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Db      10934  GCAAGTCTCCCTCCCACTTACCCCTTCCAGCAGACGGTCTGCTGACGCTTCCA 10933
Oy      139   rGlyArgValTyrrAlaAlaAspPro 147
Db      10994  CGAGCAACGCTTCCGACGTGCCT 11018

RESULT 14
US-08-764-233A-1
; Sequence 1, Application US/08764233A
; Patent No. 5716849
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Schupp, Thomas
; APPLICANT: Beck, James J.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Neff, Snezana
; APPLICANT: Ryals, John A.
; TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08764,233A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 1506/CIP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Sorangium cellulosum
; IMMEDIATE SOURCE:
; CLONE: p98/1, pU13, and pVKM15
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 383..760
; OTHER INFORMATION: /product= "Sora"
; OTHER INFORMATION: /note= "This gene encodes a protein that is highly homologous
; OTHER INFORMATION: the reductase domains of type I PKSs such as eryA from
; OTHER INFORMATION: Saccharopolyspora erythraea."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 927..19874
; OTHER INFORMATION: /product= "Sora"
; OTHER INFORMATION: /note= "Gene product is highly homologous to type I PKSs that
; OTHER INFORMATION: are known to be involved in the synthesis of polyketide

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? OTHER INFORMATION: compounds..
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 942..7115
? OTHER INFORMATION: /product= "Module 1 of SorA"
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 7203..12884
? OTHER INFORMATION: /product= "Module 2 of SorA"
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 13455..19616
? OTHER INFORMATION: /product= "Module 3 of SorA"
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 19871..46318
? OTHER INFORMATION: /product= "SorB"
? OTHER INFORMATION: /note= "Gene product is highly homologous to type I PKS gene"
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 19870..24556
? OTHER INFORMATION: /product= "Module 1 of SorB"
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 24638..30820
? OTHER INFORMATION: /product= "Module 2 of SorB"
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 30881..35446
? OTHER INFORMATION: /product= "Module 3 of SorB"
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 35528..40114
? OTHER INFORMATION: /product= "Module 4 of SorB"
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 40190..46318
? OTHER INFORMATION: /product= "Module 5 of SorB"
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 46851..47891
? OTHER INFORMATION: /product= "SorM"
? OTHER INFORMATION: /note= "The protein encoded by the sorM gene is highly homologous to the methyltransferase from Streptomyces"
? OTHER INFORMATION: homologous to the methyltransferase from Streptomyces
? OTHER INFORMATION: hygroscopicus that is involved in the synthesis of the
? OTHER INFORMATION: polyketide rappamycin."
US-08-764-233A-1

Alignment Scores:
Pred. No.: 214 Length: 49377
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545A-2_COPY_1_148 (1-148) x US-08-764-233A-1 (1-49377)
QY 47 SerGlyProSerSerLeuValTYrThrSerAlaMetProGlyPheProTYrProAlaAla 66
DB 27009 AGCGGGCTCTCGAGATGAGGCGATGCTTCTCCGTCGAGGTCAGGCCCAATCCGCTCTCA 27068
QY 67 ThrAlaAlaAlaAlaTYr---ArgGlyAlaHis-LeuArgGlyArgGlyValrghrValTY 85
DB 27069 CGCTCGGGCTCCGGGAGACCTGGGAGCGGCTCACCGCTCGATTCGTCGCTCGCTCA 27128
QY 85 rAsnThrPheArgAlaAlaAlaAlaPProPProPProAlaAlaTYrGlyGlyValValTY 105
DB 27129 TTCGACG---AGAGAGAGGCGCACCTCGCCGCTGCTCTCTCTCGGCGGAGCTCTCTA 27185
QY 105 rGlnGlnPProValTYrGlyValnLysLeuLeuGlnGlyGlyTYrAlaAlaAlaTYrArgTYrAl 125
DB 27186 CCGGAGGCT-----CGCGCTCGACTGGAAGGACTTCTTCGCGCCCTCAGGCTCCCC 27236

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: January 30, 2004, 16:58:29 ; Search time 21 Seconds
(without alignments)
298.191 Million cell updates/sec

Title: US-09-809-545a-2_COPY_1_148
Perfect score: 148
Sequence: 1 MTNKKAVNPYINGWKLNPV.....PATMAAYSDSYGRVYADPY 148

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_Aa:*
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2: /cgn2_6/prodata/1/1aa/5B COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B COMB.pep:*
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6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	57	38.5	330	3	US-09-145-391-2	Sequence 2, Appl1
2	13	8.8	366	3	US-09-176-657-2	Sequence 2, Appl1
3	13	8.8	366	4	US-09-421-299-2	Sequence 2, Appl1
4	8	5.4	325	4	US-09-702-705-1816	Sequence 1816, Appl
5	8	5.4	325	4	US-09-736-457-1816	Sequence 1816, Appl
6	8	5.4	342	3	US-09-043-937A-2	Sequence 2, Appl1
7	8	5.4	882	3	US-09-413-814-78	Sequence 78, Appl
8	7	4.7	7	2	US-08-666-473-13	Sequence 13, Appl
9	7	4.7	11	2	US-07-814-220-5	Sequence 5, Appl1
10	7	4.7	11	2	US-07-812-421-5	Sequence 5, Appl1
11	7	4.7	11	4	US-09-117-121-2	Sequence 2, Appl1
12	7	4.7	20	2	US-07-814-220-27	Sequence 2, Appl1
13	7	4.7	20	2	US-07-812-421-27	Sequence 2, Appl1
14	7	4.7	21	2	US-07-814-220-24	Sequence 24, Appl
15	7	4.7	21	2	US-07-812-421-24	Sequence 24, Appl
16	7	4.7	25	2	US-07-814-220-33	Sequence 33, Appl
17	7	4.7	25	2	US-07-812-421-33	Sequence 33, Appl
18	7	4.7	28	2	US-07-814-220-36	Sequence 36, Appl
19	7	4.7	28	2	US-07-812-421-36	Sequence 36, Appl
20	7	4.7	33	4	US-09-117-121-3	Sequence 3, Appl1
21	7	4.7	38	4	US-09-117-121-16	Sequence 16, Appl
22	7	4.7	38	4	US-09-117-121-24	Sequence 24, Appl
23	7	4.7	38	4	US-09-117-121-26	Sequence 26, Appl
24	7	4.7	38	4	US-09-344-529-5	Sequence 5, Appl1
25	7	4.7	39	4	US-09-117-121-18	Sequence 18, Appl
26	7	4.7	39	4	US-09-117-121-20	Sequence 20, Appl
27	7	4.7	39	4	US-09-117-121-22	Sequence 22, Appl

28	7	4.7	39 4	US-09-117-121-28	Sequence 28, Appl
29	7	4.7	39 4	US-09-117-121-32	Sequence 32, Appl
30	7	4.7	39 4	US-09-117-121-35	Sequence 35, Appl
31	7	4.7	39 4	US-09-117-121-36	Sequence 36, Appl
32	7	4.7	54 4	US-09-117-121-30	Sequence 30, Appl
33	7	4.7	63 2	US-08-700-013B-2	Sequence 2, Appl1
34	7	4.7	63 2	US-08-700-013B-4	Sequence 4, Appl1
35	7	4.7	76 6	5496550-6	Patent No. 5496550
36	7	4.7	96 3	US-08-465-343A-11	Sequence 11, Appl
37	7	4.7	98 2	US-07-814-220-2	Sequence 2, Appl1
38	7	4.7	98 2	US-07-812-421-2	Sequence 2, Appl1
39	7	4.7	105 4	US-09-191-468-104	Sequence 104, App
40	7	4.7	105 4	US-09-191-468-106	Sequence 106, App
41	7	4.7	105 4	US-09-191-468-108	Sequence 108, App
42	7	4.7	105 4	US-09-191-468-110	Sequence 110, App
43	7	4.7	105 4	US-09-191-468-112	Sequence 112, App
44	7	4.7	105 4	US-09-191-468-114	Sequence 114, App
45	7	4.7	105 4	US-09-191-468-116	Sequence 116, App

ALIGNMENTS

```
RESULT 1
US-09-145-391-2
; Sequence 2, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/145,391
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-145-391-2

Query Match      38.5%; Score 57; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.1e+49;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      49 PSSLVYTSAMPGEPPYPAATMAAAYRGAGHLRGRGRTVYNTFRRAAPPPIPAYGVVY 105
Db      244 PSSLVYTSAMPGEPPYPAATMAAAYRGAGHLRGRGRTVYNTFRRAAPPPIPAYGVVY 300

RESULT 2
US-09-176-657-2
; Sequence 2, Application US/09176657
; Patent No. 6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guejler, Karl J.
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176,657
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
```

FEATURE: -
OTHER INFORMATION: 1250374
US-09-176-657-2

Query Match 8.8%; Score 13; DB 3; Length 366;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RGAHLRGRGRTVY 85
DB 267 RGAHLRGRGRTVY 279

RESULT 3
US-09-421-299-2
Sequence 2, Application US/09421299
Patent No. 6524579
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Aina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/421,299
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: 09/176,657
EARLIER FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 366
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 1250374
US-09-421-299-2

Query Match 8.8%; Score 13; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RGAHLRGRGRTVY 85
DB 267 RGAHLRGRGRTVY 279

RESULT 4
US-09-702-705-1816
Sequence 1816, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1816
LENGTH: 325
TYPE: PRT

ORGANISM: Homo sapiens
US-09-702-705-1816

Query Match 5.4%; Score 8; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPI 97
DB 67 AAAPPPI 74

RESULT 5
US-09-736-457-1816
Sequence 1816, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1816
LENGTH: 325
TYPE: PRT
ORGANISM: Homo sapiens
US-09-736-457-1816

Query Match 5.4%; Score 8; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPI 97
DB 67 AAAPPPI 74

RESULT 6
US-09-043-937A-2
Sequence 2, Application US/09043937A
Patent No. 6211432
GENERAL INFORMATION:
APPLICANT: BOUDET, ALAIN-MICHEL
PICHON, MAGALIE
GRIMA-PETTEMATI, JACQUELINE
BECKER, MICHEL
GAMAS, PASCAL
BRIAT, JEAN-FRANCOIS
TITLE OF INVENTION: DNA SEQUENCES CODING FOR CINNAMOYL-CoA
REDUCTASE, AND APPLICATIONS THEREOF IN THE CONTROL OF
LIGNIN CONTENTS IN PLANTS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE, P.C.
STREET: 110 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,937A
FILING DATE: 24-Jul-1998
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR96/01544
FILING DATE: 03-OCT-1996
APPLICATION NUMBER: FR 95.11623
FILING DATE: 03-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-043-937A-2

Query Match 5.4%; Score 8; DB 3; Length 342;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 PAATAAA 71
DB 2 PAATAAA 9

RESULT 7
US-09-413-814-78
Sequence 78, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloeker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or
TITLE OF INVENTION: heteropolypeptide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 78
LENGTH: 882
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-413-814-78

Query Match 5.4%; Score 8; DB 3; Length 882;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 89 RAAAPPP 96

DB 336 RAAAPPP 343

RESULT 8
US-08-666-473-13
Sequence 13, Application US/08666473
Patent No. 5843713
GENERAL INFORMATION:
APPLICANT: YOSHIDA, Aruto
APPLICANT: TAKEUCHI, Makoto
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-SEP-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-22101
FILING DATE: 09-FEB-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-269111
FILING DATE: 01-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/837
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-666-473-13

Query Match 4.7%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 PAATAAA 70
DB 1 PAATAAA 7

RESULT 9
US-07-814-220-5
Sequence 5, Application US/07814220
Patent No. 5925540
GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toch, Thomas E.
APPLICANT: Szumanski, Maria B.W.

TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitlam, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-814-220-5

Query Match 4.7%; Score 7; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATAAA 71
|||
Db 2 AATAAA 8

RESULT 10
US-07-812-421-5
Sequence 5, Application US/07812421
Patent No. 5932697
GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitlam, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-5

Query Match 4.7%; Score 7; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATAAA 71
|||
Db 2 AATAAA 8

RESULT 11
US-09-117-121-2
Sequence 2, Application US/09117121
Patent No. 6307020
GENERAL INFORMATION:
APPLICANT: Hew, Choy
APPLICANT: Gong, Zhiyuan
TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
TITLE OF INVENTION: and Nucleic Acids
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA97/00062
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 016252-001610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-117-121-2

Query Match 4.7%; Score 7; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATAAAA 71
1 AATAAAA 7

RESULT 12
US-07-814-220-27
Sequence 27, Application US/07814220
Patent No. 5925540

GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toch, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/568,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT. 016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-814-220-27

Query Match 4.7%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATAAAA 71
9 AATAAAA 15

RESULT 13
US-07-812-421-27
Sequence 27, Application US/07812421
Patent No. 5932697
GENERAL INFORMATION:

APPLICANT: Caceci, Thomas
APPLICANT: Toch, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/568,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT. 016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-27

Query Match 4.7%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATAAAA 71
9 AATAAAA 15

RESULT 14
US-07-814-220-24
Sequence 24, Application US/07814220
Patent No. 5925540
GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toch, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitlam, Michael E.
REGISTRATION NUMBER: 32,635
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-814-220-24

Query Match 4.7%; Score 7; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATPAAA 71
|||
8 AATPAAA 14

Db

RESULT 15
US-07-812-421-24
Sequence 24, Application US/07812421
Patent No. 5932697
GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toch, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITLAM, CURTIS & WHITLAM
STREET: Reston Int'l. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitlam, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-24

Query Match 4.7%; Score 7; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATPAAA 71
|||
8 AATPAAA 14

Db

Search completed: January 30, 2004, 17:02:59
Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 30, 2004, 16:58:29 ; Search time 34 Seconds

(Without alignments)
904.646 Million cell updates/sec

Title: US-09-809-545A-2_COPY_1_148

Perfect score: 148

Sequence: 1 MTNKKAVNPYTNMGWKLNPV.....PATAAYSDSYGRVYAADPY 148

Scoring table: OLIGO

Gapco 60.0 , Gapext 60.0

Searched: 789580 seqs, 207824079 residues

Word size : 0

Total number of hits satisfying chosen parameters: 789580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	203	10	US-09-809-545A-2
2	57	38.5	330	9	US-09-794-591-2
3	13	8.8	366	12	US-10-359-385-2
4	13	8.8	450	10	US-10-094-749-1926
5	8	5.4	325	10	US-09-736-457-1816
6	8	5.4	325	10	US-09-902-941-1816
7	8	5.4	325	10	US-09-849-626-1816
8	8	5.4	325	10	US-10-113-872-1816
9	8	5.4	325	12	US-10-382-600-28
10	8	5.4	325	15	US-10-017-754-1816
11	8	5.4	342	9	US-09-833-790-236
12	8	5.4	342	15	US-10-177-293-246
13	8	5.4	340	15	US-10-207-653-198
14	8	5.4	633	14	US-10-086-464-11
15	8	5.4	674	15	US-10-156-761-9618

16	8	5.4	708	12	US-10-382-600-29	Sequence 29, Appl
17	7	4.7	19	9	US-09-864-761-35418	Sequence 35418, A
18	7	4.7	72	9	US-09-864-761-33368	Sequence 33368, A
19	7	4.7	92	10	US-09-966-546-24	Sequence 24, Appl
20	7	4.7	92	10	US-09-966-545-24	Sequence 24, Appl
21	7	4.7	92	11	US-09-965-232-24	Sequence 24, Appl
22	7	4.7	92	12	US-10-189-940-24	Sequence 24, Appl
23	7	4.7	105	16	US-10-191-813-104	Sequence 104, App
24	7	4.7	105	12	US-10-191-813-106	Sequence 106, App
25	7	4.7	105	12	US-10-191-813-108	Sequence 108, App
26	7	4.7	105	12	US-10-191-813-110	Sequence 110, App
27	7	4.7	105	12	US-10-191-813-112	Sequence 112, App
28	7	4.7	105	12	US-10-191-813-114	Sequence 114, App
29	7	4.7	105	12	US-10-191-813-116	Sequence 116, App
30	7	4.7	105	12	US-10-191-813-118	Sequence 118, App
31	7	4.7	116	9	US-09-867-550-1068	Sequence 1068, App
32	7	4.7	117	12	US-10-029-386-33868	Sequence 33868, A
33	7	4.7	132	9	US-09-864-761-37187	Sequence 37187, A
34	7	4.7	133	14	US-10-062-254-150	Sequence 150, App
35	7	4.7	147	9	US-09-864-761-38175	Sequence 38175, A
36	7	4.7	157	10	US-09-764-864-1325	Sequence 1325, App
37	7	4.7	189	9	US-09-810-264-20	Sequence 20, Appl
38	7	4.7	203	12	US-10-258-666-6	Sequence 6, Appl
39	7	4.7	203	15	US-10-158-761-13350	Sequence 13350, A
40	7	4.7	221	10	US-09-738-626-5334	Sequence 5334, App
41	7	4.7	261	15	US-10-043-487-220	Sequence 220, App
42	7	4.7	263	15	US-10-156-761-9572	Sequence 9572, App
43	7	4.7	272	12	US-10-174-209-24	Sequence 24, Appl
44	7	4.7	282	15	US-10-102-806-478	Sequence 478, App
45	7	4.7	287	15	US-10-176-847-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-809-545A-2
; Sequence 2, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS 017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-809-545A-2

Query Match 100.0%; Score 148; DB 10; Length 203;
Best Local Similarity 100.0%; Pred. No. 3.6e-127;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTNKKAVNPYTNMGWKLNPVGAAYSPDFAAGTYLLCQANQEGSSMYSGPSSLYTTSAMRG 60
DB	1	MTNKKAVNPYTNMGWKLNPVGAAYSPDFAAGTYLLCQANQEGSSMYSGPSSLYTTSAMRG 60
QY	61	FPYPATTAATAAARGAHLRGGRVTNTPFAAAPPPPIAYGVVYQEPYGNKLLGGYA 120
DB	61	FPYPATTAATAAARGAHLRGGRVTNTPFAAAPPPPIAYGVVYQEPYGNKLLGGYA 120
QY	121	AYRYAQTPTATAAAYSDSYGRVYAADPY 148
DB	121	AYRYAQTPTATAAAYSDSYGRVYAADPY 148

RESULT 2
US-09-794-591-2

; Sequence 2, Application US/09794591
; Patent No. US20010018198A1
; GENERAL INFORMATION:
; APPLICANT: Puilec, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/794,591
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/145,391
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-591-2

Query Match 38.5%; Score 57; DB 9; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.8e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 PSSLVYTSANPEFPYPATAAAYRGALHGRGRTVNTFPAAPPPPIPGGVY 105
DB 244 PSSLVYTSANPEFPYPATAAAYRGALHGRGRTVNTFPAAPPPPIPGGVY 300

RESULT 3
US-10-359-385-2
; Sequence 2, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guesgler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PP-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-10-359-385-2

Query Match 8.8%; Score 13; DB 12; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 RGAHLRGRGRTVY 85
DB 267 RGAHLRGRGRTVY 279

RESULT 4
US-10-094-749-1926
; Sequence 1926, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1926
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1926

Query Match 8.8%; Score 13; DB 12; Length 450;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 73 RGAHLRGRGRTVY 85
DB 341 RGAHLRGRGRTVY 353

RESULT 5
US-09-736-457-1816
; Sequence 1816, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1816
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1816

Query Match 5.4%; Score 8; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 90 AAAPPEPI 97

Db 67 AAAPPPPI 74

RESULT 6

US-09-902-941-1816
; Sequence 1816, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darriek
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1816
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-1816

Query Match 5.4%; Score 8; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPPI 97
Db 67 AAAPPPPI 74

RESULT 7

US-09-849-626-1816
; Sequence 1816, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaltanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1816
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-1816

Query Match 5.4%; Score 8; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 90 AAAPPPPI 97
Db 67 AAAPPPPI 74

Db 67 AAAPPPPI 74

RESULT 8

US-10-113-872-1816
; Sequence 1816, Application US/10113872
; Publication No. US20030170255A1
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleach, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113,872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1816
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-113-872-1816

Query Match 5.4%; Score 8; DB 12; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPPI 97
Db 67 AAAPPPPI 74

RESULT 9

US-10-382-600-28
; Sequence 28, Application US/10382600
; Publication No. US20030219799A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; APPLICANT: Eber, Reinhard
; TITLE OF INVENTION: Cancer-Linked Gene as Target for Chemotherapy
; FILE REFERENCE: 689290.127
; CURRENT APPLICATION NUMBER: US/10/382,600
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/362,419
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-382-600-28

Query Match 5.4%; Score 8; DB 12; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPPI 97
Db 67 AAAPPPPI 74

RESULT 10
US-10-017-754-1816
; Sequence 1816, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:

```

; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McInabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1816
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-754-1816

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Query Match      5.4%; Score 8; DB 15; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 90 AAAPPPI 97
Db 67 AAAPPPI 74

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RESULT 11
US-09-833-790-236
; Sequence 236, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Monamath, Rachodh
; APPLICANT: Indirias, Carol Y.
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.512
; CURRENT APPLICATION NUMBER: US/09/833,790
; CURRENT FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-790-236

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Query Match      5.4%; Score 8; DB 9; Length 342;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 90 AAAPPPI 97
Db 84 AAAPPPI 91

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RESULT 12
US-10-177-293-246
; Sequence 246, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen

```

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; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Matic, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MFI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-246

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Query Match      5.4%; Score 8; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 90 AAAPPPI 97
Db 84 AAAPPPI 91

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RESULT 13
US-10-207-655-198
; Sequence 198, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-198

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Query Match      5.4%; Score 8; DB 15; Length 540;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 64 PAATAAA 71
 Db 484 PAATAAA 491

Db 308 RAAAPPP 315
 Search completed: January 30, 2004, 17:01:53
 Job time : 42 secs

RESULT 14
 US-10-086-464-11
 ; Sequence 11, Application US/10086464
 ; Publication No. US20020199218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GORING, Daphne R. et al.
 ; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
 ; FILE REFERENCE: P 25, 762-A USA
 ; CURRENT APPLICATION NUMBER: US/10/086,464
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 10/069,304
 ; PRIOR FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: PCT/CA00/00966
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/149,466
 ; PRIOR FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: US 60/159,122
 ; PRIOR FILING DATE: 1999-10-13
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 633
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-086-464-11

Query Match 5.4%; Score 8; DB 14; Length 633;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 SSMYSGPS 50
 Db 245 SSMYSGPS 252

RESULT 15
 US-10-156-761-9618
 ; Sequence 9618, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMTURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 9618
 ; LENGTH: 674
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 US-10-156-761-9618

Query Match 5.4%; Score 8; DB 15; Length 674;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 89 RAAAPPP 96

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